### STIC-Biotech/ChemLib

129789

From:

Yaen, Christopher

Sent:

Thursday, August 12, 2004 2:59 PM

To:

STIC-Biotech/ChemLib

Subject:

09/889300

could you run a regular search and an interference search on seq id 1 and 2

thanks

Christopher Yaen US Patent Office Art Unit 1642 571-272-0838 REM 3A20 REM 3C18 UR (F)

STAFF USE ONLY

Searcher:\_\_\_\_\_
Searcher Phone: 2Date Searcher Picked up:\_\_\_
Date Completed:\_\_
Searcher Prep/Rev. Time:\_\_\_

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Type of Search

NA Sequence: #\_\_\_\_\_\_

AA Sequence : #\_\_\_\_\_\_

Structure: #\_\_\_\_\_\_

Bibliographic:

Litigation: \_\_\_\_\_\_

Patent Family: \_\_\_\_\_\_\_

Other: \_\_\_\_\_\_

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Vendors and cost where applicable
STN:
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QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

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se write a detailed statement of search topic. Describe s s that may have a special meaning. Give examples or re	levent citations, authors, keywo	ords, etc., if known. For sequences,
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August 16, 2004, 11:08:06; Search time 50.4574 Seconds (without alignments) 649.568 Million cell updates/sec
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1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1. geneseqp.1980s:\*
2. geneseqp.1990s:\*
3. geneseqp.2000s:\*
5. geneseqp.2001s:\*
6. geneseqp.2001s:\*
7. geneseqp.2003bs:\*
8. geneseqp.2003bs:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Res

	Description		Aab10443 Murine mo	Aaw49814 Amino aci	Abr55869 Anti-glyc	Aar39266 Mouse C4G	0	Aaw01580 Lead bind	Aae34367 Escherich	Abg71533 Mouse ant		Aar12238 Mouse MAD	Aar09427 ME4 Heavy	MAb	Aaw85063 Mouse ME4	7	ın	Aaw49813 Amino aci	ന	Aaw07437 Anti-DNA	Aar39267 Humanised	Aaw49817 Fragment	Aar39268 Humanised	Aaw49818 Amino aci	871	Aar43339 Completel
	Д		AAB10443	AAW49814	ABR55869	AAR39266	AAW49810	AAW01580	AAE34367	ABG71533	AAR12360	AAR12238	AAR09427	AAW06216	AAW85063	ABU58897	AAW34515	AAW49813	ABR55868	AAW07437	AAR39267	AAW49817	AAR39268	AAW49818	ABR55871	AAR43339
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Sequence 116 AA;

Aaw49816 Amino aci

2 AAW49816

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Abg71534 Mouse ant Aap70624 Sequence		Aaw10584 Anti-hepa	Aaw16340 Mouse-hum	Aaw41054 Human ant	Aaw47510 Human ant	Aaw47517 Human ant	Aaw89535 Chimeric	Aab98085 Chimeric	Adc65003 Human imm	Aar88716 Mouse ant	Abg71536 Mouse ant	Ade52216 E3Bi prot	Ade52217 pG1EN-EH3	Ade52214 pG1EN-EH3	Aaw00557 Nematode	Aaw43913 Mus muscu	Aaw01585 Lead bind	Aaw00833 Variable
ABG71534 AAP70624	AAW10239	AAW10584	AAW16340	AAW41054	AAW47510	AAW47517	AAW89535	AAB98085	ADC65003	AAR88716	ABG71536	ADE52216	ADE52217	ADE52214	AAW00557	AAW43913	AAW01585	AAW00833
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502.5	498.5	498.5	498.5	498.5	498.5	498.5	498.5	498.5	498.5	497.5	497.5	497.5	497.5	497.5		492	490.5	490.5
26		29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

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This invention describes the novel use of an antibody targeted to a human cellular membrane antigen, to manufacture a medicament to prophylactically vaccinate against cancer. The antibodies against tumor associated antigen (TAA) for prophylactic and/or therapeutic vaccination against cancer may be used in low doses (when compared to antibodies against TAA for passive immunotherapy), typically less than 1 mg by injection. The antibodies also have a long continual activity that directly induces immunity and their shelf life is unlimited (Iresh vaccination is always possible). This sequence represents the murine monoclonal antibody MAK HEZ variable region heavy chain fragment which is used in the method of the invention
                                                                                                                                        s; monoclonal antibody; MAK HE2; heavy chain; variable region; cellular membrane antigen; tumor associated antigen; TAA; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel use of antibodies against human cellular membrane antigens vaccination against cancer.
                                                                                                        Murine monoclonal antibody MAK HE2 variable region heavy chain.
             AAB10443 standard; protein; 116 AA
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                                                                                                                                                                                                                                                                                                       12-JAN-2000; 2000WO-EP000174.
                                                                                                                                                                                                                                                                                                                                        99CH-00000051.
                                                                            (first entry)
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                                                                           01-DEC-2000
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                                              AAB10443;
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AAB10443
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for

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ABR55869;
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                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
                                                                                                9
                                                                                                                                                                                                                                                                                                                                                          Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; caute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                  1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                      QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                            61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
                                                                                                                                               NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
                                         Gaps
                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
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               Length 116;
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/note= "complementarity determining
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               DB 3;
             100.0%; Score 614; DB 3;
100.0%; Pred. No. 8e-47;
ive 0; Mismatches (
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92US-00895952.
92US-00944159.
93US-00059159.
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               Query Match
Best Local Similarity 100.
Matches 116; Conservative
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11-SEP-1992;
03-MAY-1993;
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extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIIb/IIIa on their surfaces, for the detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; glycoprotein Ilb/IIIa; monoclonal antibody; human; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-glycoprotein IIb/IIIa MAb mature heavy chain variable region.
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form truncated glycan, and adding or deleting glycosyl groups to a
peptide and/or adding modifying group of a peptide to remodel the
                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                               Length 119;
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19-OCT-2001; 2001US-0344692P.

28-NOV-2001; 2001US-033423F.

07-JUN-2002; 2002US-0334301F.

17-JUN-2002; 2002US-039177F.

17-JUN-2002; 2002US-0395694F.

16-AUG-2002; 2002US-0396594F.
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                                                                                                                                                                              Sequence 119 AA;
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us-09-889-300a-1.rag

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Factor IX peptide, follicle stimulating hormone peptide, erythropotetin (BPO) peptide, granulocyte macrophage colony stimulating factor (GW-CSF) peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-FI) peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA) ceceptor/immunoglobulin (19 G fusion peptide, urokinase peptide, anti-ceptor/immunoglobulin (19) G fusion peptide, urokinase peptide, anti-captide, anti-day peptide, anti-captide, chimeric anti-fier anti-body peptide, receptide, common (MSV) F peptide, anti-colonal antibody peptide, anti-captide, chimeric anti-fier insulin peptide, hepatitis B surface antigen (HbAQ), human growth common (HGH) peptide, and a modifying group, where the modifying group, as covalently attached to the peptide through an intact glycosyl linking remodeling the above mentioned peptides. The present sequence represents and anti-glycoprotein Ilb/IIIa monoclonal antibody mature heavy chain
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monoclonal antibody; platelet agglutination; humanised antibody.
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/label= complementarity_determining_region_1
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|Tabel= signal_peptide
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|abel=light_chain
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92US-00895952.
92US-00944159.
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/label=_CDR_2
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/label= CDR_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.6
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse C4G1 Ig heavy-chain
                                                                                                                                                                                                                                                                                           Sequence 119 AA;
                                                                                                                                                                                                                                                           variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9313133-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L5-DEC-1992;
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29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1992;
11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR39266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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AAR39266
       \begin{array}{c} \mathbb{R} \\ \mathbb{R} \\ \mathbb{R} \\ \mathbb{R} \end{array}
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This is the sequence of the mouse C4G1 immunoglobulin heavy chain. See AAR32265 for the light chain sequence. The antibody is specific for the GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                             61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                             NEKFKGKATLIYDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWPAYWGRCTLVIVSA 138
                                                              psn. contg. immunoglobulin specific for the GP-IIB and -IIIA protein treating disorders related to vascular thrombosis.
                                                                                                                                                                                                                                                                                          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                          20 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEMVKQRPGQGLEWIGVIYPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse, antibody C4G1, heavy chain, humanised; immunoglobulin; Ig; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction, unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                 θ,
                                                                                                                                                                                                                                       Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // note= "mature proter...
50. .54
/note= "complementarity determining region"
69. .85
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118. .127
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable region of mouse antibody C4G1 light chain.
                                                                                                                                                                                                                                     Score 554.5; DB 2;
Pred. No. 1.8e-41;
3; Mismatches 4;
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.138
.e= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                     Disclosure; Fig 2B; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW49810 standard; protein; 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                   Query Match 90.3%;
Best Local Similarity 91.6%;
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                        WPI; 1993-227275/28.
                                    N-PSDB; AAQ45663
                                                                                                                                                                                                             Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-1995;
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24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW49810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
Co MS,
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AAE3436
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                                                                                                                                            This is the amino acid sequence of the mouse antibody C4G1 heavy chain, used in the method of the invention involving the creation of a humanised immunoglobulin (IG) derived from the mouse C4G1 antibody. The humanised IG is capable of binding to GPIID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The IG can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acutem myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIID/IIIa on their surfaces, for the detection of GPIID/IIIa antigens or for isolating platelets. (Updated on 25-MAR-2003 to correct PA field.)
                                                                            New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                          61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NEKFKGKATLITVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 138
                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cosmetic;
herbicide;
                                                                                                                                                                                                                                                                                                                                   DB 2; Length 138;
                                                                                                                                                                                                                                                                                                                                   Score 554.5; DB 2; Length 1
Pred. No. 1.8e-41;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody, Fd fragment, lead cation, perfume, pharmaceutical, health care, skin treatment; pesticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lead binding MAb 14F11 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW01580 standard; protein; 119 AA
                                                                                                                           Disclosure, Fig 2B; 35pp; English
(YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murray PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00462798.
95US-00541373.
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.6%;
Matches 109; Conservative
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                                           WPI; 1998-398136/34.
N-PSDB; AAV36742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wylie DE, Lopez O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-043140/04.
N-PSDB; AAT58254.
                                                                                                                                                                                                                                                                                                             Sequence 138 AA;
                        Co MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9639518-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy metal
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The present sequence represents the heavy chain variable region for monoclonal antibody (MAD) 14F11, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cometics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NEKFKCKATLTADKSSSTAYMOLSSLTSDDSAVYFCARDGP---WFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCARSGYGHWYFDVWGAGTTVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.0%; Score 546.5; DB 2; Length 119;
89.9%; Pred. No. 7.7e-41;
tive 3; Mismatches 6; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim CS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE34367 standard; protein; 138 AA
                                                                                                                       Claim 12; Page 63; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50. .66
/note= "CDR2"
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/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee JW, Ko IY, Kang HK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31. .35
/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 119 AA;
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                                                                       cations.
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Region
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New light and heavy chain variable regions of a monoclonal antibody against the S-surface antigen of the hepatitis B virus (HBV), useful for neutralizing or removing HBV, or for preventing or treating HBV
                                                                                                                                                               The invention relates to light and heavy chain variable regions of a monoclonal antibody against S-surface antigen of the hepatitis B virus (HBV). The variable regions of the antibodies are useful against HBV S-surface antigens, e.g. adr. adw, arr or ayw, particularly for neutralising or removing HBV. They may also be employed to treat or prevent HBV. Integers the present sequence is Escherichia coli heavy
                                                                                                                     Claim 12; Page 17; 20pp; English.
                                                                                                                                                                                                                                                                                                         chain variable region
                                                                                                                                                                                                                                                                                                                                                          Sequence 138 AA;
                                                                       infection
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61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCA-----RDGPWFAYWGQGTLVTV 114 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 1 QVQLQQSGTEMVRPGTSVKVSCKASGYPFTNHLIEWVKQRPGQPEWIGVINPGSGGTNY 61 NEKEKGKATLTADKSSSTAYMQLNSLTSDDSAVYFCAIMTTFLGEGYAMDYWGQGTSVTV Gaps 84.5%; Score 519; DB 6; Length 138; ilarity 83.6%; Pred. No. 2.46-38; Conservative 5; Mismatches 9; Indels Similarity SA 116 SS 122 102; 115 121 Query Match Local Matches g ò  $\stackrel{>}{\circ}$ g

9 9

> Mouse anti-acetyllysine monoclonal antibody (mAb) heavy chain #1 ABG71533 standard; protein; 164 AA. (first entry) 31-DEC-2002 ABG71533; RESULT 8 ABG71533

Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine; functional analysis; acetyllysine-containing protein; pathosis; acetylated protein; disease disapnosis; histone acetylation; mab; antibody-producing immortalised cell; heavy chain.

Mus sp.

WO200274962-A1. 26-SEP-2002. 13-MAR-2002; 2002WO-JP002330.

2001JP-00074263. 15-MAR-2001;

(NISC-) JAPAN SCI & TECHNOLOGY CORP. (NIHA ) JAPAN ENERGY CORP.

Komatsu Y, Yoshida M;

WPI; 2002-750555/81. N-PSDB; ABS55467. Production of anti-acetyllysine monoclonal antibody capable of recognizing Napproximatelyi-acetyllysine regardless of types of adjacent amino acids, useful in e.g. disease diagnosis and searching for novel acetyllysine-containing proteins.

Example 4; Fig 4; 45pp; Japanese

The present invention relates to a mouse anti-acetyllysine monoclonal antibody (mAb) capable of recognising N epsilon-acetyllysine, and a method for producing the monoclonal antibody. The produced antibody is useful in searching for and functional analysis of novel acetyllysine. Containing proteins particularly in studying pathosis due to acetylated proteins, disease diagnosis, facilitating detection of variation in acetylation levels of histone influenced by various stimulations during western blotting, analysis of the variable region in the DNA sequence of an antibody gene of an antibody-producing immortalised cell, and judging the degree of homology specific to the sequence during the protein translation. The monoclonal antibody of the invention is capable of recognising N epsilon-acetyllysine regardless of the type of adjacent amino acids and accepting adjacent amino acids over a broad range. The present sequence represents a heavy chain of mouse anti-acetyllysine mAb

Ś

Sequence 164 AA; 

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                                                                                                                                                                                                     NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                               NEKFKGKATLTADISSSTAYMOLSSLTSEDSAIYYCARSDYYGSWFAYWGOGTLVTVSA 119
                                                                                                     QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                    1 OVOLOOSGAELVRPGTSVKMSCKAAGYTFTNHWIGWVKQRPGHGLEWIGDIYPGSGYTNY
                                                         ب
ب
/ Match 84.3%; Score 517.5; DB 5; Length 164; Local Similarity 84.0%; Pred. No. 4e-38; les 100; Conservative 6; Mismatches 10; Indels 3;
                                                                                                                                                                                                     61
       Query Match
                                 Best Loca
Matches
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Heavy chain variable region of murine 4D12 immunoglobulin. Ź AAR12360 standard; protein; 137 (revised)
(first entry) 25-MAR-2003 15-AUG-1991 AAR12360; AAR12360 ID AAR1 XX RESULT

89US-00433730. 13-NOV-1989; 13-NOV-1989; WO9107493-A. 30-MAY-1991 

Chimeric antibodies; immunoconjugates; HIV; AIDS

Mus musculus

89US-00433730. (XOMA ) XOMA CORP. (GREC ) GREEN CROSS CORP

Ghoshdasti P, Robinson R; Horwitz AH, Better MD,

WPI; 1991-178105/24. N-PSDB; AAQ12062. New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample.

Disclosure, Fig 17; 107pp; English.

This is the heavy - chain variable (V) region of a mouse monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 4D12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined

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WPI; 1990-115825/15
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nes 102; Conserv
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                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1988;
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04-OCT-1988;
19-JUN-1989;
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by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also AAQ12056-61 and AAQ12063. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                          NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                                                                                                                                                                             NEKEKDKITMTADKSSSTAYMHLDSLISDDSAVYLCARIGSGHALEYWGQGISVIVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
                                                                                                                                                                                                     QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                                                                                           Length 137;
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                                                                                                                                                         12; Indels
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83.9%; Score 515; DB 2;
Best Local Similarity 84.7%; Pred. No. 5.5e-38;
Matches 100; Conservative 4; Mismatches 12;
                                                                                                                           Score 515; DB 2;
Pred. No. 5.5e-38;
4; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 17; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                            AAR12238 standard, protein; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse MAb 4D12 H chain V region.
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                                                                                                                             83.9%;
al Similarity 84.7%;
100; Conservative
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(first entry)
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                                                                                                                                Query Match
Best Local Similarity
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                                                                                                    Sequence 137 AA;
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19-AUG-1991
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Matches 1
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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

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The sequence is used in the prodn. of a chimeric antibody mol, comprising two light chains and two heavy chains, each having a constant region (muth) and a variable region (mutine) having specificity to an antigen bound by mutine monoclonal antibody (MAb) B38.1. The chimeric antibodies can be used for any purpose for which the original mutine MAbs can be body. They are esp. that they are more compatible with the human body. They are more compatible with the human body. They are sep. used for the diagnosis and treatment of cancer. (Updated on 25-MAR-2003 to correct PA field.)
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20 QVHLQOSGABMVRPGTSVKVSCRASGYAFTNYLIEWVKQRPGGGLEWIGVINPGSGGTTX 79
                                                                              61 NEKFKGKATLTADKSSSTAYMOLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                         80 NEKFKDKTTMTADKSSSTAYMHLDSLTSDDSAVYLCARTGSGHALEYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 OVOLOOSGAELVRPCTSVKVSCTTSGYAFTNYLMEWMKORPGOGLEWIGVINPGSGDAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 515; DB 2;
Pred. No. 5.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric mouse-human antibodies - prepd. using human region murine variable region, esp. to 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen; diagnosis; cancer; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ME4 Heavy Chain V Region (mouse).
                                                                                                                                                                                                                                                                   AAR09427 standard; protein; 141
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88US-00253002.
89US-00367641.
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85.0%;
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(first entry)
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us-09-889-300a-1.rag

(revised)

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20-MAR-2003
16-APR-1999
        AAW85063;
The heavy chain variable region (AAW06216) of mouse monoclonal antibody ME4 is the product of a CDNA clone (AAT4341) isolated from a ME4 hybridoma cDNA library. MAD ME4 (1931) binds to an antigon that is expressed on the surface of human lung, breast, colon and ovary carcinomas and melanomas, but not on most normal adult tissues. The heavy chain and light chain variable regions (see also AAW06219) of ME4 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chimeric antibodies (see also AAW06209-14 and AAW06217-18) can the treatment and diagnosis of human cancer. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                    Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                       Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.9%; Score 515; DB 2; Length 141;
85.0%; Pred. No. 5.6e-38;
ive 4; Mismatches 10; Indels
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                                                                                     MAb ME4 heavy chain variable region.
                AAW06216 standard; protein; 141 AA
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                                                                                                                                                                                                                              88US-00240624.
88US-00241744.
88US-00243739.
88US-00253002.
89US-00367641.
                                                                                                                                                                                                                                                                                                                                   Lei S, Better MD,
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                                                                 (first entry)
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                                                         (revised)
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N-PSDB; AAT43441.
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                                                                                                                                                                                                            27-DEC-1994;
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                                                       25-MAR-2003
13-FEB-1997
                                                                                                                                                                    US5576184-A.
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13-SEP-1988
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                                    AAW06216;
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Matches
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The present sequence represents the heavy chain variable region of murine amtibody ME4. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytotoxifity to purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEKFKGKATITADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                Heavy chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody; treatment; human cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric antibody specific for human tumour antigen - useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.9%; Score 515; DB 2;
85.0%; Pred. No. 5.6e-38;
iive 4; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoassay, imaging or antitumour agent
                                              Mouse ME4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 30; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                88US-00240624.

8RUS-00241744.

8RUS-00241739.

8US-00253002.

89US-00367641.

89US-00382768.

89WO-US003852.

91US-006594011.
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(first entry)
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Best Local Similarity 85.0 Matches 102; Conservative
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06-SEP-1989;
06-MAY-1991;
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19-JUN-1989;
                                                                                                                                                                                                                                 US5843685-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-1994;
                                                                                                                                                                                                                                                                             01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU58897;
                                                                                                                                                                                  Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
ABUS8897
ID ABUS8
XX
AC ABUS8
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116

79

20 QVQLQQSGABLVRPGTSVKVSCTTSGXAFTNYLMBWMKQRPGQGLEWIGVINPGSGDAKY 61 NEKFKGKATLTADKSSTAYMQLSSLTSDSAVYFÇARD--GPWFA--YWGQGTLVTVSA

ga 25

NENFKGKATLTADKSSSTSYMQLSSLTSDDSAVYFCARGHYGGYFVMDYWGQGTSVTVSA 139

80

AAW85063 standard; protein; 141 AA

RESULT 13 AAW85063 ID AAW850

Mouse; human tumour antigen; anti-human tumour antigen-antibody; ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis; tumour therapy; cytostatic; heavy chain variable region.

Mouse antibody heavy chain variable region #4.

(first entry)

16-APR-2003

```
Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody.
                                                                                                                                                Example 3; Fig 30; 101pp; English.
                                                                                                                     2003-196707/19.
                                                                                                                     WPI; 2003-196707,
N-PSDB; ABK79242
                                                                                                                                                                                                                                                                     Sequence 141 AA;
```

The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the ING-1 antibody, where the ING-1 is produced by cell line HB9812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an immunasasy method for detecting an antigen in a sample by contacting a label and relating the detected label to the presence of the antigen; for use in an inaging method for revealing the presence of the antigen; for use in an inaging method for revealing the presence of a label-detectable antigen in an animal by contacting the antibody with a part of the animal subspected of containing the antigen, detecting the label and relating the carrying an antigen by contacting the calls with the antibody and allowing the killing to cocur. The antibodies are useful in tumour dispension and therapy. The chimeric antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothelial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human tumour cell lines combined with minimal reactivity with normal tissues imply that these antibodies may mediate selective destruction of antigent contains antibodies may mediate selective destruction of antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains an antigent contains an antigent contains and antigent contains and antigent contains an antigent contains and antigent contains and antigent contains and antigent contai maintaint closure into presence of mannary action that man articular determinants on the chimeric antibodies increases their resistance to rapid clearance from the body relative to the original murine mAbs. This resistance to clearance enhances the potential utility of these chimeric antibodies, as well as their derivatives, in tumour diagnosis and therapy. This is the amino acid sequence of a mouse antibody heavy chain variable region used in the creation of an anti-human tumour antigen-

This sequence represents the variable heavy chain of the antibody produced by hybridoma 5-465-210, and can be detected using the method of the produced by hybridoma 5-465-210, and can be detected using the method of the presence of antibody which may be present in a test sample. It comprises contacting a test sample suspected of containing the antibody with an antigen specific for the cuspected of containing the antibody with an antigen specific for the engloying as a control or calibrator, a reagent which binds to the employing, as the control or calibrator, a reagent which binds to the antibody constant region epitopes, where the reagent binds to the antigen and is homogeneous with respect to specificity and affinity. The method can be also be used for detecting the presence of antibodies developed against more than one antigen. The method is used particularly for the detection of human antibodies specific for a given antigen, e.g. HIV-1. Hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all of the problems associated with using an immune sera in the manufacture of clanbractors and positive controls. The present reagents can be readily and reproducibly generated in virtually unlimited quantities and are also useful for quantitating, and monitoring the integrity of, the antigen

Score 515; DB 6; Pred. No. 5.6e-38; 83.9%; 85.0%; Query Match Best Local Similarity

Length 141;

Score 510.5; DB 2; Length 138; Pred. No. 1.4e-37;

83.1%; 84.9%;

Query Match Best Local Similarity

Sequence 138 AA; used in assays

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ζ,
                                                     116
                                                                09
                                  19
                                                                                                                                                                                                                                                                                                                                                                                  Use of antibody constant region epitope(s) - as control or calibrator reagents in assays for detecting the presence of an antibody in a test
                 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                               20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSGDAKY
                                                     61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA
Gaps
                                                                                                                                                                                            Variable region coding sequence; constant region epitope; hybridoma; antibody detection; antigen/antibody complex; variable heavy chain.
4,
                                                                                                                                                                          Variable heavy chain of antibody from hybridoma 5-465-210.
Indels
10;
                                                                                                                                                                                                                                                                                                                                     Golden AM;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 60; 109pp; English.
                                                                                                                      AAW34515 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                     Ostrow DH,
                                                                                                                                                                                                                                                                               97WO-US001074.
                                                                                                                                                                                                                                                                                                  96US-00589939.
                                                                                                                                                          (first entry)
 102; Conservative
                                                                                                                                                                                                                                                                                                                                    Hackett JR, Hoff JA,
                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-393833/36.
                                                                                                                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT98832
                                                                                                                                                          19-MAR-1998
                                                                                                                                                                                                                                          WO9727486-A1.
                                                                                                                                                                                                                                                                                17-JAN-1997;
                                                                                                                                                                                                                                                                                                  23-JAN-1996;
                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                            31-JUL-1997.
                                                                                                                                         AAW34515;
 Matches
                                                                                                    RESULT 15
                                                                                                              AAW34515
                                                                                                                               음
                                                       8
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Chang CP;

Lei S,

Robinson RR,

88US-00243739. 89US-00367641. 89US-00382768. 89WO-US003852,

13-SEP-1988 04-OCT-1988 91US-00659401 94US-00364001

27-DEC-1994;

19-JUN-1989 21-JUL-1989 06-SEP-1989 (XOMA ) XOMA TECHNOLOGY LID.

Better MD, Horwitz AH,

95US-00467142 88US-00240624 88US-00241744

06-JUN-1995;

US6461824-B1.

08-OCT-2002.

Matches	101;	Matches 101; Conservative	ς, ,	5; Mismatches 10; Indels	10;	Indels	3;	3; Gaps	ı,
ò	0-	VOLOOSGAELVRPGTSV	KVSC	KASGYAFTNYLIE	WVKOR	PGOGLEWIG	VINPG	SGGINY	09
qa	20 07	20 QVHLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVTQRPGQGLEWIGVINPGSDFTYY 79	- KVSC	KASGYAFTNYLIE	WVTOR	PGOGLEWIG	VINPG	SDFTYY	4
ζ	61 NE	61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQCTLVTVSA 116	AYMO	LSSLTSDDSAVYF	CAR	-DGPWFAYW	GOGTL	VTVSA 1	16
QD	- N	KFKGRATITADKSSS	- NY A'		OPPTT	-     -   -   -   -   -   -   -   -   -	- E	1.TVSS 1	α

Search completed: August 16, 2004, 11:12:17 Job time : 51.4574 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - pr	OM protein - protein search, using sw model
Run on:	August 16, 2004, 11:08:06; Search time 46.5426 Seconds (without alignments) 649.568 Million cell updates/sec
Title:	US-09-889-300A-2
Sequence:	1 NIVMTQSPKSMSMSVGERVTCGQGYSYPYTFGGGTKLEIK 107

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Total number

Searched:

seq length: 0 seq length: 200000000 Minimum DB a

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\* A Geneseq 29Jan04:\* 1: 'geneseqp1980s:\* geneseqp2004s:\* geneseqp1990s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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uo	Mouse J59	J5.91 mono	Monoclona	Murine mo 1E6 kappa	Mouse J59	J591 mono	Murine mo	MAb 10.1	Mouse ant	Hybridoma	Hybridoma-	Mouse 09	Ber-H2 he	Mouse AF2	Murine AF	Variable	Variable	Murine J4	Murine J4	Variable	Variable	Murine J4	Murine J4	Murine J4
script	1 40	Aay90374	Aab36225	Aar27144	Aaw47085	Aay90370	Aab36222	4	Abg74248	Abr82783	Abr82893	Abb07176	Aaw01632	Aay71545	Aab69693	Aaw00828	Abo10727	Abr44618	Abr44671	Abo10737	Abo10738	Abr44682	Abr44624	Abr44622
	P P P P P P P P P P P P P P P P P P P																							
SUMMARIES	AAW47086	AAY90374	AAB36225	44	AAW47085	AAY90370	AAB36222	AAW01145	ABG74248	ABR82783	ABR82893	ABB07176	AAW01632	AAY71545	AAB69693	AAW00828	ABO10727	ABR44618	ABR44671	AB010737	ABO10738	ABR44682	ABR44624	ABR44622
DB	2	01	N 0	n (7	~1	2	(1	~1	9	7	7	'n	(7)	ო	4	C)	φ	9	9	v	Q	Q	9	9
Length	. 0	0	107	109	121	121	121	127	132	135	135	101	136	127	136	108	107	107	107	107	ō		ō	107
% Query Match	100	100.0	000	100.0	00	0	00	0	$\circ$	0	O	S	m	S	7	90.6	σ	9	σ	~	~	~	87.2	r-
Score	562	562	262	562	562	562	562	562	562	562	562	534	527	521	521	509	503	503	503	490	490	490	490	4 90
Result No.	1	01.0	<b>™</b> <	* 10	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Murine J4	Variable	Murine J4	Murine J4	Variable	Murine J4	Murine J4	Consensus	Variable	Variable	Murine J4	Murine J4	Murine J4	5 Murine J4	Murine J4	Murine J4	ScFv anti	Variable	0 Murine J4	Murine J4
m	Abo10739	Abr44625	Abr44683	Abo10736	Abr44680	Abr44621	Abo10741	Abo10729	Abo10740	Abr44684	Abr44623	Abr44626	Abr44685	Abr44617	Abr44673	Aar64812	Abo10735	Abr44620	Abr44679
ω	ABO10739	ABR44625	ABR44683	ABO10736	ABR44680	ABR44621	ABO10741	ABO10729	ABO10740	ABR44684	ABR44623	ABR44626	ABR44685	ABR44617	ABR44673	AAR64812	ABO10735	ABR44620	ABR44679
9	9	ω	Q	9	9	ø	9	9	9	ø	છ	9	9	9	ø	7	Ģ	ø	9
101	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	239	107	107	107
	86.7	86.7	86.7	86.3	86.3	86.3	9	86.1	86.1	86.1	86.1	86.1	86.1	86.1					85.1
490	487	487	487	485	485	485	484	484	484	484	484	484	484	484	484	482	478	478	478
				30	31		33	34	32	36	37	38	en en	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

AAW4	AAW47086 ID AAM47086 standard, mostein, 107 AA
ž	scandard, Processi,
AC	AAW47086;
ξE	ofTIN-loss (first entry)
i ×	
DE	Mouse J591 monoclonal antibody light chain variable region.
X	,
ΚX	Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
<b>3</b>	cancer; vascular endothelial cell; metastatic adenocarcinoma.
50	,
3 \$	ילים מחיי
Z Z	W09803873-A1.
X	
В	29-JAN-1998.
×	
면	17-JUL-1997; 97WO-US012035.
×	
PR	18-JUL-1996; 96US-0022125P.
PR	09-APR-1997; 97US-00838682.
X	
PA	(CORR ) CORNELL RES FOUND INC.
×	
PI	Bander NH;
X	
DR	WPI; 1998-120937/11.
DR	N-PSDB; AAV13952.
×	
F	Destroying cancer cells with agent that binds to prostate specific
PŢ	membrane antigen - on vascular endothelial cells near the cancer, or on
ΡŢ	ypertrophic or cancerous prostatic cells, also us
L.	diagnosis.

Example 12; Page 60; 94pp; English.

The present sequence represents the mouse U591 monoclonal antibody light chain variable region from an example of the present invention. The present invention describes the elimination of cancer cells by treating vascular endothelial cells (UEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC (Dese to, or within, a cancer cancer cancer cancer cells eliminating or detecting normal, benignly hyperplastic or cancercous prostate epithelial cells using optionally labelled (A); (3)

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The method is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds to an epitope of PSMA expressed on live cells (contrast antibody 7E11 which only binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Both cancer cells themselves and the VEC on which they depend are killed. All VEC close to cancer cells express PSMA, whatever the type of cancer, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is a fragment of the light chain of the monoclonal antibody 291. The invention relates to an isolated antibody or its antison binding portion (I) which binds to an extracellular domain of prostate specific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign
                                                                                                                                                                                                                                                                                                                                                                                                                  9
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hybridomas that produce a monoclonal antibody (MAb) that binds to PSMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIVMIQSPKSMSMSVGERVTLICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or normal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U591 monoclonal antibody, extracellular domain, diagnosis, therapy, prostate specific membrane antigen, prostate cancer, light chain.
                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J591 monoclonal antibody light chain protein sequence fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                          100.0%; Score 562; DB 2; Length 107; 100.0%; Pred. No. 4.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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96US-0022125P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-120937/11.
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                        normal VEC do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA37834.
                                                                                                                                                                                                                                                                                    Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1996;
18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6107090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bander NH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis
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hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic agents. (I) targets only prostate epithelial cells and other tissue are spared which provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these antibodies are more effective than those which target lysed prostate
                                                                                                                                                                                                                                                                                                                                                                         1 NIVMIQSPKSMSMSVGERVTLICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or on
                                                                                                                                                                                                                                                                                                                                                                                                            1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, conormal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; antibody; heavy chain; prostate cancer; biological agent.
                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                     Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody J591 kappa light chain V region #1.
                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                   Score 562; DB 2;
Pred. No. 4.1e-39;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36225 standard; protein; 107 AA
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                                                                                                                                                                                                                                                                                                   100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0016976P.
96US-0022125P.
97US-00838682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00895914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-120937/11.
N-PSDB; AAC66544.
                                                                                                                                                                                                                                                                                                                      Local Similarity
les 107; Conserv
                                                                                                                                                                                                                                                                  Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2001
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                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                          Matches
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NIVMTOSPKSMSWGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes the novel use of an antibody targeted to a human callular membrane antigen, to manufacture a medicament to prophylactically and/or therapeutically vaccinate against cancer. The antibodies against tumor associated antigen (TRA) for prophylactic and/or therapeutic vaccination against cancer may be used in low doses (when compared to antibodies against TRA for passive immunotherapy), typically less than 1 mg by injection. The antibodies also have a long continual activity that directly induces immunity and their shelf life is unlimited (fresh vaccination is always possible). This sequence represents the which is used in the method of the invention
                                                                                                                               9
                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                      Murine, monoclonal antibody, MAK HE2, light chain, variable region,
human cellular membrane antigen, tumor associated antigen, TAA, vaccine,
an antibody which may be used as the biological agent of the invention. In addition to prostate cancer, the method can be used with renal, urothelial, colon, renal, lung and breast cancer cells, and cancerous cells of metastatic adenocarcinoma to the liver
                                                                                                                                                  1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                            1 NIVMTOSPKSMSWGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel use of antibodies against human cellular membrane antigens for
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                                                                                                                                                                                                                                                                                                                              Murine monoclonal antibody MAK HE2 variable region light chain.
                                                                                                                                                                                          61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                            61 RFIGSGSAIDFILIISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                 Length 107;
                                                                                                       0; Indels
                                                                              100.0%; Score 562; DB 2;
100.0%; Pred. No. 4.1e-39;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 562; DB 3; 100.0%; Pred. No. 4.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 47-48; 54pp; German.
                                                                                                                                                                                                                                                            AAB10444 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-2000; 2000WO-EP000174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99CH-00000051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccination against cancer.
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                           Best Local Similarity LUU.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loibner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IGEN-) IGENEON GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-475956/41.
                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200041722-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-1999;
                                                                                                                                                                                                                                                                                                         01-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eckert H,
                                                                                                                                                                                                                                                                                  AAB10444;
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                                                                               Query Match
Best Local §
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Best Local Similarity 100. Matches 107; Conservative

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Light and heavy chain variable region sequences were deduced from the DNA sequences obtd. by PCR of DNA sequences obtd. from the hybridoma cell line lE6-2012 (ATCC HB 10693). The light and heavy chain regions may be used to construct a monoclonal antibody active against LPA-3 which blocks adhesion of LFA-3 expressing cells to lymphocytes. The antibody may be used in the treatment and diagnosis of acute and chronic inflammation, autoimmune diseases and for immuno- modulation including systemic lupus erythematosus, rheumatoid arthritis and thyroiditis. See also AAR27145s. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibodies active against lymphocyte function associated antigen-3 - for treating inflammation and auto:immune diseases, and detecting LFA-3 protein in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric, heavy chain; variable region; monoclonal antibody; lymphocyte function associated antigen-3; LFA-3; inflammation; autoimmune disease; immunomodulation; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                               Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                1E6 kappa light chain variable region.
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                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; thyroiditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 14; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wallner
                                                                                                                                                                                                                                                  AAR27144 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92EP-00104318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00667975
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .97
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89. .97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                   (revised)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ28653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
20-MAY-1998
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                                                                                                                                                                                                                                                                                                  AAR27144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
domain
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1 NIVMIQSPKSMSMSVGERVTLICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60 

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Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            J591 monoclonal antibody, extracellular domain; diagnosis; therapy; prostate specific membrane antigen; prostate cancer; kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                     J591 monoclonal antibody kappa light chain protein sequence #1.
                                                                                                                             61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                           67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                       AAY90370 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC.
  107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-120937/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA37832
                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-1997;
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18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS6107090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bander NH;
                                                                                                                                                                                                                                                                                                                                   AAY90370;
  Matches
                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                AAY90370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the mouse J591 monoclonal antibody light chain from an example of the present invention. The present invention describes the elimination of cancer cells by treating vascular endothelial cells (VEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the derection of cancer tissue by detecting binding of labelled (A) to VEC close to, or within, a cancer tissue; (2) climinating or detecting normal, benighly hyperplastic or cancerous prostate epithelial cells using optionally labelled (A); (3) hybridoms that produce a monoclonal antibody (MAD) that binds to PSMA. The method is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the epitope of PSMA expressed on live cells (contrast antibody 7E11 which only binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Both cancer cells themselves and the VEC on which they depend are killed. All VEC on the VEC on which they depend are killed. All VEC on the VEC on which they depend are killed. All VEC on the VEC on the VEC on the type of cancer, but
Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                                                                                                                                             Mouse, monoclonal antibody, J591; prostate specific membrane antigen, cancer; vascular endothelial cell; metastatic adenocarcinoma.
                                                                                          61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                        Mouse J591 monoclonal antibody light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Page 57; 94pp; English.
                                                                                                                                                                                                                        AAW47085 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0022125P.
97US-00838682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US012035.
                                                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; AAV13951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9803873-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-1996;
09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1997;
                                                                                                                                                                                                                                                                                                              26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bander NH;
                                                                                                                                                                                                                                                                  AAW47085;
                                                                                                                                                                                                   AAW47085
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97US-00838682. 96US-0016976P. 96US-0022125P.

(first entry)

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This sequence is the kappa light chain of the monoclonal antibody J591. The invention relates to an isolated antibody or its antigan binding portion (I) which bind does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplastic, and cancerous epithelial cells or portrions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for eg. recurrence of prostatic disease. They can also be used patient for e.g. recurrence of prostate concer. They can also be used epithelial cells as a therapy for prostate cancer. Sinding and internalishing of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cyclocxic antigen, permits the therapeutic use of intracellularly acting cyclocxic antigen, permits the therapeutic use of intracellularly acting cyclocxic antigen, permits character epithelial cells and other tissue are spared which provides after readment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these artiphodies are more effective than those which target lysed prostate
Example 12; Fig 10; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 121 AA;
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Score 562; DB 2; Length 121; Pred. No. 4.7e-39;

100.0%;

Query Match Best Local Similarity

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Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, crebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and collits. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3U1 (P3xSAPAB, U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture eupernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CLAB. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly
                                                                                                                                                                                                           Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis; cerebral infarction; eaute Kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody inhibiting type II phospholipase A2 activity - for treatment of myocardial and cerebral infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKFEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                            MAb 10.1 light chain, directed against type II phospholipase A2.
   RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 562; DB 2;
100.0%; Pred. No. 4.9e-39;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        suitable for preclinical testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 13; 69pp; Japanese.
                                                                               AAW01145 standard; protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                        44. 54
/label= CDR 1
70. 76
/label= CDR 2
                                                                                                                                                                                                                                                                                                                                                                                                       109. .117
/label= CDR 3
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                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takasaki J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawauchi Y,
                                                                                                                                               10-FEB-1997
                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9620959-A1
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   63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method of killing cancer cells, particularly prostate cancer cells, by directing a biological agent to the cells which then binds to a prostate specific membrane antigen and causes the molecule to be internalised. The internalisation of the agent, which may be bound to a drug or which may act to kill the cell alone, then leads to the death of the cell. The present sequence forms part of an antibody which may be used as the biological agent of the invention. In addition to prostate cancer, the method can be used with renal, urchhalial, colon, renal, ung and breast cancer cells, and cancerous cells of metastatic adenocarcinoma to the liver
                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                            7 NIVMTQSPKSMSMSVGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYIGVPD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                               1 NIVMTQSPKSMSWGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or normal, hypertrophic or cancerous prostatic cells, also used for
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                      Mouse; antibody; heavy chain; prostate cancer; biological agent.
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                0; Indels
                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                       Murine monoclonal antibody J591 kappa light chain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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   4.7e-39;
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
 Pred. No.
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                                                                                                                                                                                                                        AAB36222 standard; protein; 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORR ) CORNELL RES FOUND INC
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0016976P.
96US-0022125P.
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                                                                                                                                                                                                                                                                                       (first entry)
                Conservative
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-1996;
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Best Local Simi
Matches 107;
               107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis.
                                                                                                                                                                                                                                                        AAB36222;
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                Matches
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Gaps

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Indels

Length 127;

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81

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RESULT 11

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CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating a human patient diagnosed with a B-cell malignancy by administering a blocking anti-CD22 monoclonal antibody binding to the first two Ig-like domains of native human CD22 (hCD22),
                                                                                                                                                                                        Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
                            ABR82783 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 32; Fig 23; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002; 2002US-0359419P.
21-OCT-2002; 2002US-0420472P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003; 2003WO-US005323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYDU-) UNIV DUKE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuscano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-712652/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACF36433.
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                                                                                                                                                                                                                                                                                                                                                       WO2003072036-A2
                                                                                                                                    18-DEC-2003
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    redder T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR82893;
                                                                                ABR82783;
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ID ABR8
XX ABR8
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ABR82783
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(ganglioside antigen) binding domain of antibody MB3.6, with any of 3

variable gene sequences, or the PSMA (prostate-specific membrane antigen)

binding domain of antibody 3D8, 4D4 and 3B11, with variable gene

equences, the zeta signalling chain of the T cell receptor and an

intervening CD8alpha hinge in which cysteine residues have been mutated.

The chimaeric molecules expressed in T cells or NK cells or other

effector cells are useful in treating patients with cancers expressing

the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3B11 derivatives),

and/or together with each other or with heterologous constructs to engage
additional stimulatory and functional properties of the effector cells to

enhance the antitumour therapeutic efficacy (claimed). They are

changed the sequence of the construct of th
                                                                                                                                                                                                                                                                                                T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3 6; PSW4; tumour; 3D8; 4D4; 3E11; prostate-specific membrane antigen; zeta signalling chain; CD81pha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; light chain variable region; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
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                                                                                                                                                                                                                                               Mouse antibody 3E11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                   ABG74248 standard; protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0250087P.
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Best Local Similarity 100.
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABX16574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002132983-A1.
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                                                                                                                                                                                           22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2002
                                                                                                                                       ABG74248;
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                            RESULT 10
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The invention relates to treating a human patient diagnosed with a B-cell malignancy. The method involves (a) administering to the human patient a blocking anti-CD22 monoclonal antibody binding to the first two 1g-like domains, or to an epitope within the first two Ig-like domains of native human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the malignancy to the treatment. The method is useful for treating a human patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma, Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy cell leukemia or prolymphocytic leukemia. The present sequence represents the amino acid sequence for kappa light chain V-J junction for anti-CD22 antibody from hybridoma HB22-196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NIVMTOSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 562; DB 7;
100.0%; Pred. No. 5.2e-39;
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Matches 107; Conservative
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neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitie
                                                                                                                                                                             (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 35A-B; 219pp; English.
                                                                                                                                                                                                                   Rodriguez M, Miller DJ, Pease LR;
                                                                                               30-MAY-2000; 2000WO-US014902.
                                                                                                                                       10-MAY-2000; 2000US-00568351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 101; Conservative
                                                                                                                                                                                                                                                           WPI; 2002-066596/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 encephalomyelitis
                                                                                                                                                                                                                                                                              N-PSDB; ABA94223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 101 AA;
                   WO200185797-A1.
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                                                           15-NOV-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW01632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to treating a human patient diagnosed with an autoimmune disease. The method involves administering to the patient an amount of a blocking anti-CD22 monoclonal antibody and monitoring the response of the autoimmune disease to the treatment. The method is useful in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis, Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or allergiess) or B-cell malignancies (e.g. tymphomas or leukemias). The present sequence represents the amino acid sequence for kappa light chain V-J junction for anti-CD22 antibody from hybridoma HB22-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating an autoimmune disease or a B-cell malignancy in a human patient comprises administering an amount of an anti-CD22 monoclonal antibody to the patient and monitoring the response of the disease to the treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 NIVWTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80
                                                CD22; autoimmune disease; anti-CD22 antibody; iImmunosuppressive; cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer; antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic; antidiabetic; antiallergic; gene therapy; HB22-196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuromodulatory, central nervous system; CNS; sHIgM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse 09 antibody kappa light chain 1 variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 562; DB 7;
100.0%; Pred. No. 5.2e-39;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 23; 69pp; English
                                                                                                                                                                                                                                                                                                                21-FEB-2002; 2002US-0359419P
21-OCT-2002; 2002US-0420472P
                                                                                                                                                                                                                                                                            21-FEB-2003; 2003WO-US005549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 100.
107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-721765/68.
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                                                                                                                                                                                              WO2003072736-A2
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   redder TF;
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The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHighZ2 (LW 22), ebwHigh Ms11910, ebv High CB2BG9, AKCR4, CB21E12, CB2HE7 or MS119ES. (I) is useful for stimulating remyelination of CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells in CNS axons, or treating demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TNEV) or for treating a human being having multiple sclerosis, or a post-neural disease of CNS. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for an in vitro method of stimulating the grain infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, and other conditions in the CNS where nerves are damaged as by trainma The present contractors are served as a patient and the causes and contex conditions and the context of the angert of the conditions and any of diseases, and other conditions and sease, and do ther conditions and seases. The disease, and conditions and the context conditions and the conditions are sease. The disease, and other conditions and the conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             damaged as by trauma. The present sequence represents the mouse 09 antibody kappa light chain 1 variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 534; DB 5; Length 101; 100.0%; Pred. No. 8e-37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFIGSGSATDFILTISSVQAEDLADYHCGQGYSYPYTFGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGG 101
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Local

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RESULT 13 ABB07176

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Search completed: August 16, 2004, 11:12:18
Job time : 47.5426 secs
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Best Local S
                            Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The ligands are useful for diagnosis or therapy of CD30 expressing cancers, esp. Hodgkinson's disease. Cytoplasmic RNA was isolated from calls of the mouse myeloma hybrid line Ber-H2. CDNA was isolated using reverse transcriptase. A VHDJ fragment contg. band was cut from a gel and purified. DNA corresponding to VK and Vgamma was isolated and cloned into vectors. Oligonucleotides used are given in AAT58331 to AAT58340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; AF2-VL; light chain variable region; VL; heavy chain variable region; VH; IgG2b; gamma-interferon; IFN; complementarity determining region; CDR; RR; framework region; immunosuppressive; antiinflammatory; antisclerotic; gastrointestinal; antidiabetic; antiarthritic; dermalogical; inhibitor; mutoimnume disease; graft versus host disease; organ transplant; multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis; systemic lupus erythematosus; SLE; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                     DNA mols. encoding CD30-specific immunoglobulin variable regions - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 NIVMTQSPRSMSMSVGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
             immunoglobulin; variable region; CDR; cancer; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NIVMTQSPKSMSMSVGERVTLITCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 527; DB 2; Length 136;
Pred. No. 4.1e-36;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse AF2 antibody light chain variable region (AF2-VL).
                                                                                                                                                                                                                                                                                    (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.

    .29
    label= sig_peptide

                                                                                    Location/Qualifiers
                                                                                                                                           /label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71545 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 15; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                       cancer diagnosis or therapy
                                                                                                                                                                                                                               95DE-01043039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%;
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                                                                                                                              .136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101; Conservative
                                                                                                                                                                                                                                                                                                                 Ziegler A, Stein H;
                                                                                                                                                                                                                                                                                                                                             WPI; 1996-507017/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 136 AA;
                                                                                                                                                                         DE19543039-C1
                                                         Homo sapiens.
                                                                                                                                                                                                                               08-NOV-1995;
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                                                                                                                                                                                                  21-NOV-1996.
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                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                Protein
                            Ber-H2
                CD30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The present amino acid sequence is the mouse AF2 antibody, light chain variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It is used for the construction of humanised version of mouse AF2 antibody HuZAF, that comprises mouse antibody AF2 complementarity determining regions (CDRs), functionally joined to the human acceptor antibody EU framework region (FR). HuZAF antibody specifically binds to and neutralises gamma-interferon (IFN). They can also block the binding of mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences that are immunogenically active in humans and remains unaffected by immune responses, that may reduce its activity or circulating half-life. HuZAF may be administered to treat autoimmune diseases such as graft versus host disease following organ transplant. Type I diabetes, multiple sclengs, rheumatoid arthritis, psoriasis, systemic lupus erythematosus (SLE), Habimatov bowel disease like, Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                          /note= "Mature mouse antibody AF2 light chain variable region (AF2-VL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-interferon for the treatment of autoimmune diseases, e.g. multiple sclerosis and diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
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                                                                                                                                                                                                                                                                     70. .76
/label= CDR
/note= "Complementarity determining region"
1109. .117
/label= CDR
/note= "Complementarity determining region"
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                                                                                                                                                                                    4. .54
|abel= CDR
note= "Complementarity determining region"
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Pred. No. 1.2e-35;
5; Mismatches 4;
                                                             note= "N-terminal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vasquez M, Landolfi NF, Tsurushita N,
iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0110523P.
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1 Similarity 91.6%;
98; Conservative 9
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                                                                                          .127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200032634-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-2000.
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Sequence 103, App Sequence 103, App Sequence 103, App Sequence 103, App Sequence 6, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 55, Appli Sequence 36, Appli Sequence 36, Appli Sequence 36, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli

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Query Match 100.0%; Score 562; DB 3; Length 107; Best Local Similarity 100.0%; Pred. No. 3.4e-50; Matches 107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-08-838-682-16
Sequence 16, Application US/08838682
Patent No. 6107090
Patent No. 6107090
CENERAL INFORMATION:
APPLICANT: Bander M.D., Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVETWALE: PREADLING SYSTEM: C-LOUS FMS-LOUS
SOFTWARE: PREADLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,682
FILING DATE: CLASSIFICATION ADMER: US/08/838,682
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
ATTONENY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISCHATION NUMBER: 30,727
REFRENCE/DOCKET NUMBER: 19603/1172
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 16:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
US-07-634-278-103
US-08-47-040-103
US-08-470-040-103
US-08-48-7-20-103
US-08-48-537-103
US-08-450-5208-6
US-09-117-370-4
US-09-118-25
US-09-118-25
US-09-118-25
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US-09-118-25
US-09-118-25
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US-08-25-370-118
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US-08-25-38-718
US-08-25-38-718
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US-08-25-38-718-15
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US-08-25-38-718-15
US-08-25-38-718-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rochester STATE: New York COUNTRY: U.S.A. ZIP: 14603-1051 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: DATE OF PERATING SYSTEM: PC-DOS/MS-DOS
  TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-682-16
  STRANDEDNESS
    Appli
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Sequence 99,
Sequence 99,
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Sequence 16,
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Sequence 11,
                                                                                                                                                                                                                                                               1 NIVMIQSPKSMSMSVGERVT......CGQGYSYPYTFGGGTKLEIK 107
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Sequence 11,
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'GGTZ 6/ptodata/2/iaa/5A COMB.pep:*
'CGTZ 6/ptodata/2/iaa/5B_COMB.pep:*
'CGTZ 6/ptodata/2/iaa/6A_COMB.pep:*
'CGTZ 6/ptodata/2/iaa/6B_COMB.pep:*
'CGTZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
'CGTZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
'CGTZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-357-707-16
US-08-838-682-11
US-08-895-914-11
US-09-377-710A-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB
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Gaps

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Sequence 16, Application US/09357710A Patent No. 6290956
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ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-357-707-16
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                                    1 NIVWIQSPKSMSMSVGERVILICKASENVTIVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
    1 NIVMIQSPKSMSMSVGERVILITCKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
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                                                                                                                        100.0%; Score 562; DB 3; Length 107; 100.0%; Pred. No. 3.4e-50;
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                                                                                                61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Bander, Neil H.

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDERS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA:
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA:
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
RAME: Goldman, Michael L.
RAME: Goldman, Michael L.
REFERENCE/DOCKET NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1173
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (716) 263-130
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
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Matches 107; Conservative
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US-08-895-914-16
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GENERAL INFORMATION:
APPLICAMT: Bander, Nail H.
TILLE OF INVENTION: TRAIMENT AND DIAGNOSIS OF PROSTATE CANCER
TILLE OF INVENTION: TRAIMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REPRENCE: Loca M. Kwasigroch: BZL 242/025
CURRENT APPLICATION NUMBER: US/09/357,710A
CURRENT PAPLICATION NUMBER: US/09/357,710A
PRIOR APPLICATION NUMBER: US/09/06
PRIOR PILING DATE: 1996-05-06
PRIOR PILING DATE: 1996-05-06
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 16
LENGTH: LOT
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TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
CURRENT APPLICATION NUMBER: US/09/357,707
CURRENT FILING DATE: 1999-07-20
FRIOR APPLICATION NUMBER: US 08/838,682
FRIOR FILING DATE: 1997-07-17
FRIOR PELING DATE: 1997-07-07
FRIOR FILING DATE: 1997-07-06-09
FRIOR FILING DATE: 1996-05-06
FRIOR FILING DATE: 1996-05-06
FRIOR FILING DATE: 1996-07-18
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Best Local Similarity 100.0
Matches 107; Conservative
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SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
FILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 121 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 107; Conservative
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Rochester
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                                                                            Sequence 2, Application PC/TUS9202044
; Sequence 2, Application PC/TUS9202044
; Sequence 2, Application PC/TUS9202044
; GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: SATO, Vicki L.
APPLICANT: WALLNER, Barbara P.
TITLE OF INVENTION: WONOCLONAL ANTIBODIES RECOGNIZING
TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: APPRESS:
ATTY: New York
STREET: New York
COUNTRY: New York
STREET: New York
STREET: New York
STREET: New York
COUNTRY: U.S.A.
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Patent No. 6107090
GENERAL INFORMATION:
APPLICANT: Bander M.D., Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDER ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDAP disk
COMPUTER: ENDAP disk
COMPUTER: ENDAP disk
COMPUTER: ENDAP PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02044
FILING DATE: 19920312
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/667,975
FILING DATE: 12-MRR-1991
FILING DATE: 12-MRR-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REFERENCE/DOCKET NUMBER: B150CIP
TELEFRAM: (212) 715-0600
TELEFRAM: (212) 715-0600
TELEFRAM: (212) 715-0673
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: AD ABLID ACIDS
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
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Matches 107; Conservative
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                                                   RESULT 5
PCT-US92-02044-2
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Sequence 11, Application US/08895914;
Patent No. 618631
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
APPLICANT: BANDER: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk.
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CUNTRY: NO.S.A.

ZIP: 14603-1051

COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBN PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA: US/08/838,682
FILING DATE: US 60/016,976
FILING DATE: US 60/016,976
FILING DATE: US 60/016,976
FILING DATE: US 60/022,125
FILING DATE: U
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100.0%; Pred. No. 3.9e-50;
tive 0; Mismatches 0;
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21 NIVMTQSPKSMYVSIGERVILSCKASENVDTYVSWYQQXPEQSPKLLIYGASNRYTGVPD 80
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Best Local Similarity 91.6%;
Matches 98; Conservative
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US-09-450-520A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus sp.
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                                                  JS-09-357-707-11
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US-09-157-10A-11
US-09-157-10A-11
Sequence 11, Application US/09357710A
Fatent No. 629056
GENERAL INFORMATION
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
TITLE REPERENCE: Lois M. Kwasigroch: BZL 242/025
CURRENT APPLICATION NUMBER: US/09/357,710A
CURRENT FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1996-07-09
PRIOR PLILING DATE: 1996-07-06
PRIOR PLILING DATE: 1996-07-06
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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             FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
PRIOR APPLICATION NUMBER: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1173
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
APPLICATION NUMBER: US 60/016,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.8
Matches 107; Conservative
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US-09-357-710A-11
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66
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GENERAL INFORMATION:
APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Landolfi, Naoya
APPLICANT: Gueen, Cary L.
APPLICANT: Protein Design Labs, Inc.
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-0081100S
CURRENT APPLICATION NUMBER: US/09/450,520A
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/110,523
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 13
SOFFWARE: Patentin Ver: 2.1
SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 562; DB 4; Length 121; Best Local Similarity 100.0%; Pred. No. 3.9e-50; Matches 107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Pred. No. 6.2e-46;
5; Mismatches 4; Indels
                                                                                JAPPLICANT: BANGER, Neil H.

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER;
FILE REPERENCE: Lois M. Kwaaigroch: BZL 242/078

CURRENT APPLICATION NUMBER: US/09/357,707

CURRENT FILING DATE: 1999-07-20

PRIOR PELING DATE: 1999-07-17

PRIOR APPLICATION NUMBER: US 08/838,682

PRIOR APPLICATION NUMBER: US 08/829,682

PRIOR APPLICATION NUMBER: US 08/829,682

PRIOR APPLICATION NUMBER: US 60/016,976

PRIOR APPLICATION NUMBER: US 60/022,125

PRIOR APPLICATION NUMBER: US 60/022,125

PRIOR APPLICATION NUMBER: US 60/022,125

SACTUMER OF SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NO 11
; Sequence 11, Application US/09357707; Patent No. 6649163
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09450520A
Patent No. 6329511
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US-08-477-728-99
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                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                  81 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 127
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Pred. No. 6.8e-46;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                            Sequence 99, Application US/07634278

Patent No. 5530101

GENERAL INFORMATION:
APPLICANT: O'Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COLINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TILEON: SELICK, Harold E.
TILEON: SELICK, Harold E.
TILEONER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 33-FEB-1999
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 33-FEB-1999
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INPOMPATION:
NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INPOMPATION:
NAMM: WARTH WAITH AND MARKENEY WAS NAME: WAITH AND WAITH WAITH AND WAITH WAITH AND WAITH WAITH WAITH WAITH AND WAITH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Townsend and Townsend Khourie and Crew
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RECISTRATION NUMBER: 30.23
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 136 amino acids
amino acid
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Best Local Similarity 91.6
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-07-634-278-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 37
                                                                                                                                                                                                                                                                                                JS-07-634-278-99
                                                                                                                                                                                                                                                       RESULT 11
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RESULT 12

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1 NIVMTOSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
Sequence 99, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: GUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              COUNTY: US
COUNTY: US
COUNTY: US
COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/477,728
FILING DATE: US-UUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 521; DB 1;
Pred. No. 6.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION 1474

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1889

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATORNEY/AGENT INFORMATION:
NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 11823-00260

TELEPHONE: (415) 326.2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION: APPLICANT: QUEEN, Cary L. APPLICANT: CO, Man Sung APPLICANT: SCHNEIDER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.7%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 136 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-477-728-99
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Best Local Similarity
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US-08-474-040-99
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30 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-484-537-99
US-08-484-537-99
Sequence 99, Application US/08484537
Patent No. 6180370
Septence No. 6180370
Septence No. Man Sung
APPLICANT: OUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: COENTIER, William P.
APPLICANT: CANDOLFI, Nicholas F.
APPLICANT: CELINGH, Rathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: 379 Lytton Avenue
STREET: 379 Lytton Avenue
CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend and Crew STREET: 379 Lytron Avenue
CITY: Palo Alto
COUTRY: Dalo Alto
CONTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 07/590,274
FILING DATE: 198-DEC 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/200,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
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amino acid
3Y: linear
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CITY: Palo Alto
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    APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and Townsend And Townsend and Townsend and Townsend and Townsend STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 99, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: COHENIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:

MEDIUN TYPE: Floppy disk
COMPUTER READBLE FORM:

MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PATENT PAPENTAN PATENT PAPENTAN PATENT PAPENTAN PATENT PATENT
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TELEPAX: (415) 326-2422
INFORMATION FOR SEO ID No: 99
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 136 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-487-200-99
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STATE: california
COUNTRY: california
COUNTRY: california
COUNTRY: state of the page disk
MEDIUM TYPE: Floppy disk
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC_COOS/MS-DOS
COMPUTER: IBM PC_COOS/MS-DOS
COMPUTER: IBM PC_COOS/MS-DOS
CONFARENT APPLICATION NATA.
PFILING DATE: BC-190
PRING APPLICATION NATA.
PATLICATION NATE: 13-DEC-190
PRING APPLICATION NATION NOTE: 13-DEC-190
PRING APPLICATION NATE: 13-DEC-190
PRING APPLICATION NATION NAT
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Search completed: August 16, 2004, 11:12:58 Job time : 14.9148 secs

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864.269 Million cell updates/sec
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1 NIVWTQSPKSMSWSVGRRVT......CGQGYSYPYTFGGGTKLEIK 107
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| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/NEG_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/NEG_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 16, Appl	Sequence 16, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 70, Appl	Sequence 19, Appl	Sequence 31, Appl	Sequence 31, Appl	Sequence 34, Appl	Sequence 21, Appl	Sequence 2, Appli	Seguence 84, Appl	Sequence 99, Appl	Sequence 84, Appl	Sequence 48, Appl
SUMMARIES	ΔΙ	US-09-929-665-16	US-09-929-546-16	US-09-929-665-11	US-09-929-546-11	US-10-010-729-70	US-10-006-773-19	US-10-372-481-31	US-10-371-797-31	US-08-779-784-34	US-10-010-729-21	US-09-992-524-2	US-10-389-417-84	US-10-452-357-99	US-10-389-155-84	US-10-160-506-48
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	% Query Match Length DB	107	107	121	121	128	132	135	135	128	101	127	136	136	136	107
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.6	95.0	92.7	91.1	91.1	91.1	89.5
	Score	562	562	562	562	562	562	562	562	554	534	521	512	512	512	503
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RESULT

US-929-665-16

Sequence 16, Application US/09929665

Publication No. USZ0030001101A1

Sequence 16, Application US/09929665

Publication No. USZ0030001101A1

APPLICANTON NO. USZ0030001101A1

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION WINERS: US/09/929,665

CURRENT APPLICATION NUMBER: US/09/929,665

PRIOR PILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: US 08/838,682

PRIOR APPLICATION NUMBER: US 60/016,976

PRIOR APPLICATION NUMBER: US 60/016,976

PRIOR APPLICATION NUMBER: US 60/016,976

PRIOR APPLICATION NUMBER: US 60/022,125

PRIOR APPLICATION NUMBER: US
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NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Mus sp.
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US-09-929-665-11

US-09-929-665-11

Sequence 11, Application US/09929665

Publication No. US2030003101A1

GENERAL INFORMATION:

ATTLE OF INVENTION:

FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024

CURRENT PELLOATION NUMBER: US/09/929,665

CURRENT PELLOATION NUMBER: US/09/929,665

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: US 08/838,682

PRIOR PELLOATION NUMBER: US 08/838,682

PRIOR PELLOATION NUMBER: US 06/016,976

PRIOR PELLOATION NUMBER: US 60/016,976

PRIOR PELLOATION NUMBER: US 60/012,125

PRIOR SEQIEN NUMBER: US 60/022,125

PRIOR PELLOATION NUMBER: US 60/012,125

PRIOR PELLOATION NUMBER: US 60/012,125
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                                                                                                                                                                             JUNEAR IN TRANSPORT NOT TREATMENT AND DIAGNOSIS OF CANCER TILE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER TILE REFERENCE: Lois M. Kwasigroch: BZL 242/028 CURRENT APPLICATION NUMBER: US/09/929,546 CURRENT FILING DATE: 2001-08-13 PRIOR APPLICATION NUMBER: US/09/929,546 PRIOR PILING DATE: 1999-07-20 PRIOR APPLICATION NUMBER: US 08/838,682 PRIOR FILING DATE: 1999-07-06 PRIOR PAPLICATION NUMBER: US 60/016,976 PRIOR FILING DATE: 1996-05-06 PRIOR FILING DATE: 1996-05-06 PRIOR APPLICATION NUMBER: US 60/022,125 PRIOR FILING DATE: 1996-07-18 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PATENTING DATE: 1906-07-18 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PATENTING DATE: 1906-07-18 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PATENTING DATE: 1000-07-18 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PATENTING DATE: 1000-07-18 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PATENTING DATE: 1000-07-18 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PATENTING DATE: 1000-07-18 NUMBER OF SEQ ID NOS: 21 SEC ID NOS:
US-09-929-546-16; Sequence 16, Application US/09929546; Publication No. US20030031673A1; GENERAL INFORMATION:
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Best Local Similarity 100.1
Matches 107; Conservative
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CRGANISM: Mus sp.
US-09-929-665-11
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APPLICANT: Rodriguez, Moses
APPLICANT: Rodriguez, Moses
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human 1gM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-11-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT APPLICATION NUMBER: 09/730,473
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 1997-01-07/79,784
PRIOR FILING DATE: 1997-01-07/79,784
PRIOR FILING DATE: 1996-08-08
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                                                67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLBIK 113
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61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMIN: TREATMENT AND DIAGNOSIS OF CANCER
TITLE REFERENCE: Lois M. Kwasigroch: BZL 242/028
CURRENT APPLICATION NUMBER: US/09/929,546
CURRENT PILING DATE: 2001-08-13
FRIOR APPLICATION NUMBER: 09/357,708
FRIOR APPLICATION NUMBER: US 08/838,682
FRIOR APPLICATION NUMBER: US 08/036,976
FRIOR APPLICATION NUMBER: US 60/016,976
FRIOR APPLICATION NUMBER: US 60/016,976
FRIOR APPLICATION NUMBER: US 60/02,125
FRIOR APPLICATION NUMBER: US 60/02,125
FRIOR APPLICATION NUMBER: US 60/022,125
FRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PARCENT NOS: 21
SOFTWARE: PARCENT NOS: 21
SOFTWARE: PARCENT NOS: 21
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100.0%; Score 562; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 107; Conservative 0; Mismatches 0;
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Publication No. US20030185827A1
GENERAL INFORMATION:
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21 NIVMTQSPKSMSMSVGERVTLTCXASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80
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Sequence 34, Application US/08779784

Sequence 34, Application US/08779784

Publication No. US20020164325A1

GRNEAL INPORMATION:
APPLICANT: Maller, David J.
APPLICANT: Miller, David J.
APPLICANT: REWYELINATION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REWYELINATION USING MONOCLONAL AUTOANTIBODIES

NUMBER OF SEQUENCES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STREET: STOOR
STREET: Miller New Jersey
                                                                                                                                                                                                                                                                                                                                                          21 NIVMTQSPKSMSMSVGERVTLTCKASENVYTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                      Query Match 100.0%; Score 562; DB 12; Length 135; Best Local Similarity 100.0%; Pred. No. 2.1e-48; Matches 107; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 31, Application US/10371797
; Publication No. 1020040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
, ORGANISM: homo sapiens
US-10-371-797-31
                 ; ORGANISM: Homo sapiens
US-10-372-481-31
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: USA
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US-10-371-797-31
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LENGTH: 135
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10S-100-06-773-19

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Publication No: US2003020297541

GENERAL INFORMATION:

APPLICANT: Tedder, Thomas F.

TITLE PERERRENE: 5405.306

CURRENT APPLICATION NUMBER: US/10/372,481

CURRENT APPLICATION NUMBER: US/10/372,481

PRIOR PILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: PCT/US03/05549

PRIOR APPLICATION NUMBER: US 60/420,472

PRIOR PILING DATE: 2002-10-21

PRIOR PILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-02-21

PRIOR PLING DATE: 2002-02-21

PRIOR PLING DATE: 2002-02-21

PRIOR PRIOR PRIOR DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                    Length 128;
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                                                                                                                                                                                                                            100.0%; Score 562; DB 14; Length 100.0%; Pred. No. 2e-48; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 107; Conservative
; SEQ ID NO 70
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-70
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; ORGANISM: Mus sp.
US-10-006-773-19
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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQRPEQSPKLLIYGASNRYTGVDD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Vasquez, Maximiliano
APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Tantushita, Naoya
APPLICANT: Tantushita, Naoya
APPLICANT: Protein Design Labs, Inc.
APPLICANT: 01908: 01809/992,524
CURRENT APPLICATION NUMBER: 09/450,520
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
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Publication No. US20040049014A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
Co. Man Sung
Schneider, William P.
Landolff, Nicholas F.
Coelingh, Kathleen L.
Selingh, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                          Query Match 95.0%; Score 534; DB 14; Best Local Similarity 100.0%; Pred. No. 9.6e-46; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 92.7%; Score 521; DB 9; Local Similarity 91.6%; Pred. No. 2.5e-44; les 98; Conservative 5; Mismatches 4;
  PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09992524 Patent No. US20020091240A1 GENERAL INFORMATION:
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COTHER INFORMATION: AF2 VL
US-09-992-524-2
                                                                              , SEQ ID NO 21

: LENGTH: 101

: TYPE: PRT

: ORGANISM: Mus musculus

US-10-010-729-21
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TYPE: PRT
ORGANISM: Mus sp.
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US-10-389-417-84
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Publication No US20030185827A1
GENERAL INPORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION NUMBER: US/10/010,729
CURRENT APPLICATION NUMBER: US/130,473
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.6%; Score 554; DB 8;
99.1%; Pred. No. 1.3e-47;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1199-1-001 CIPA
                                                                                                                                                                                                             CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084

FILING DATE: 08-AUG-1956
PRIOR APPLICATION NUMBER: US 08/236,520

FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 1199-1-001

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal
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Best Local Similarity 99.1:
Matches 106; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-779-784-34
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30 NIVWIQSPKSMYVSIGERVILSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYIGVHD 89
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) Publication No. US20030229208A1
GENERAL INFORMATION:
Co. Man Sung
Schneider, William P.
Landolfi, Wicholas F.
Coelingh, Rathleen L.
Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: COUNTRY: San Francisco
STREET: TWO Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: USA
ZIP: 94111-3834
COMPUTER: READABLE FORM:
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 136;
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APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512; DB 12;
Pred. No. 2.1e-43;
5; Mismatches 5;
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APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: AF2 light chain antibody US-10-452-357-99
                 PRICE APPLICATION NUMBER: 09/718, 993
PRICE FILING DATE: 2000-11-22
PRICE FILING DATE: 2000-11-22
PRICE FILING DATE: 1995-06-07
PRICE FILING DATE: 1995-106-07
PRICE FILING DATE: 1990-12-19
PRICE APPLICATION NUMBER: 07/590,275
PRICE APPLICATION NUMBER: 07/590,275
PRICE APPLICATION NUMBER: 07/590,275
PRICE FILING DATE: 1990-09-28
PRICE FILING DATE: 1990-09-13
PRICE FILING DATE: 1990-02-13
PRICE FILING DATE: 1998-02-13
PRICE FILING DATE: 1998-12-28
NUMBER: 07/290,975
PRICE FILING DATE: 1998-12-28
NUMBER: 07/290,975
PRICE FILING DATE: 1988-12-28
SOFTWARE: PATENTING DATE: 1988-12-28
SOFTWARE: PATENTING DATE: 1988-12-28
     CURRENT FILING DATE: 2003-05-30
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l Similarity 90.7%;
97; Conservative
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ORGANISM: Artificial
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US-10-389-155-84
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Best Local S:
Matches 97
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Publication No. US20040058414A1
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
APPLICANT: Co. Man Sung
APPLICANT: Co. Man Sung
APPLICANT: Schnedder, William
APPLICANT: Schnedder, William
APPLICANT: Schnedder, Marchen
APPLICANT: Selick, Harcld
ITLLE OF INVENTION: Improved Humanized Immunoglobulins
FILE REPERENCE: 05882.0078.CNUS01
CURRENT APPLICATION NUMBER: US/10/452,357
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OEMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                    CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TBLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
91.1%; Score 512; DB 12;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/325,000
RELING DATE: 01-UN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-PEB-1969
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-UNN-1995
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                         ZIP: 94111-3834
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Sequence 48, Application US/10160506
Publication No. US20030161832A1
GENERAL INFORMATION
APPLICATE INFORMATION
ITTLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
ITTLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
ITTLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
ITTLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
ITTLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
CURRENT APPLICATION NUMBER: 06/324,100
PRIOR APPLICATION NUMBER: 60/324,100
PRIOR PILING DATE: 2002-05-30
PRIOR PLING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 128
SOFTWARE: FRAESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 48
ILENGTH: 107
TYPE: PRIOR
TYPE: PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.1%; Score 512; DB 15; Length 136; Best Local Similarity 90.7%; Pred. No. 2.1e-43; Matches 97; Conservative 5; Mismatches 5; Indels
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APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 136 amino acids
| TYPE: amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| MOLECULE TYPE: protein
| SEQUENCE DESCRIPTION: SEQ ID NO: 84:
| US-10-389-155-84
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US-10-160-506-48
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein August 16, 2004, 11:08:06; Search time 11.5157 Seconds (without alignments) 893.780 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-889-300A-2 562 1 NIVMTQSPKSMSMSVGERVT......CGQGYSYPYTFGGGTKLEIK 107

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	kappa chain	kappa chain	kappa chain	kappa chain	light chain	kappa chain	light chain	Ig light chain V r	:i-DNA autoan	kappa chain	kappa c	kappa chain	kappa chain	:i-idiotypic	kappa chain	kappa chain	light chain	kappa chain	kappa chain	lambda ch	kappa chain V	kappa chain	ppa chain V						
SUMMAKIES																														
SCO.	ID								PH1071													F30534		$\sim$	10	~	A47159	~		
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kappa	-6 antibody	light chain	kappa chain		kappa chain	kappa chain	light chain								
B28195	JC2270	826336	H38601	PL0263	PC1214	PL0083	S52793	PT0356	B49047	840317	S31981	K4HULN	B37266	841393	PT0407
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107	113	109	100	113	134	108	129	118	108	129	109	114	111	112	113
70.1	70.1	69.8	8.69	69.8	9.69	69.3	69.2	69.1	68.9	68.5	68.3	68.3	68.1	68.1	68.1
394	394	393	392	392	391	389.5	389	388.5	387	385	384	384	383	382.5	ci.
30	31	35	33	34	35	36	37	38	9	40	41	42	43	44	45

## ALIGNMENTS

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Ig Kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Date: 16-Sp-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: Plo268
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUD: 90111618; PMID: 2104919
A;Accession: PL0268
A;Molecule trype: mRWA
A;Residues: 1-107 < SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;123/Region: framework 1
F;16-90/Domain: immunoglobulin homology < INM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
              ger
A; Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated A; Reference number: A33932; MUID:892823; PMID:2499887
A; Accession: 133932
A; Accession: 133932
A; Accession: 133932
A; Residual type: mRNA
A; Residual type: mRNA
A; Residual: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 39-113/ Domain: immunoglobulin homology < INM>
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
C.Accession: S.38713
R.Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A.Reference number: S.38713
A.Accession: S.38713
A.Accession: S.38713
A.Status preliminary
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology < IMM>
F.i6-90/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                     Length 118;
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                                                                                                                                                                                                                                                                                                                                                     Query Match 88.6%; Score 498; DB 2; L
Best Local Similarity 100.0%; Pred. No. 4.8e-37;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.9%; Score 494; DB 2;
88.8%; Pred. No. 9.8e-37;
tive 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYP
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Best Local Similarity 88.8<sup>3</sup>
Matches 95; Conservative
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Cypecies: Mus musculus (house necess)
Cypecies: Wus musculus (house mouse)
Cypecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
Cyaccession: 833132
Ry Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Marc submitted to the EMBL Data Library, May 1993
A) Reserve number: 833132
A) AAccession: 833132
A) AAccession: 833132
A) Accession: 833132
A) Assatues: preliminary
A) Accession: 833132
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A) Accession: 833132
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Cype: DNA
A) Residues: 1-107 < TEM>A) Accession: 107 < TEM>A) Accession: 107 < TEM>A) Accession: 100 < TEM
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.Species: Mus musculus (house mouse)
.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: I33932
R;Baccala, R; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DIVMTQIPKSMSMSVGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYIGVPD
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R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Pred. No. 9.9e-42;
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Pred. No. 1.4e-38;
"**emarches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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Best Local Similarity 92.5°
Matches 99, Conservative
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Best Local Similarity
Matches 105; Conserva
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anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C; Accession: FD0204
R; Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1998
A; Tile: Variable region primary structures of monoclonal anti-DNA autoantibodies from P A; Reference number: PL0204
A; Rolecule type: MRNA
A; Residues: 1-108 <SMI>
A; Cross-references: OB: S55644, NID: 950198; PIDN: CAA37695.1; PID: 9930144
A; Molecule type: mRNA
A; Residues: 1-108 <SMI>
A; Cross-references: OB: S55644, NID: 950198; PIDN: CAA37695.1; PID: 9930144
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 6-90/Domain: immunoglobulin homology cIMM>F; 24.34/Region: complementarity-determining 2
F; 50-56/Region: complementarity-determining 3
F; 96-108/Region: UH region
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                                          1 SPKSMSMSVGERVTLSCKASENVGTYVSWYQQKP-QSPQLLIYGASNRYTGVPDRFTGSG 59
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Peb-1995 #sequence_revision 06-Peb-1995 #text_change 21-Jan-2000
C;Accession: 332192
R;Izui, S.
Submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIWHQSQKEMSTSVGDRVSVTCKASQNVNTYVAWYQQKPGQSPKALIYSASSRYTGVPD
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <INM>
   7 SPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSG
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76.9%; Score 432; DB 2;
Best Local Similarity 79.4%; Pred. No. 2.8e-31;
Matches 85; Conservative 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 78.3%; Score 440; DB 2; Similarity 79.4%; Pred. No. 5.5e-32; 85; Conservative 9; Mismatches 13.
                                                                                                                                                                                    60 SATDFILTISSVQAEDLADYHCGOSYSYPFTF
                                                                                                                            67 SATDFTLTISSVQAEDLADYHCGQGYSYPYTF
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A;Accession: $32192
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <1ZU>
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Best Local Similarity
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PH1071
Ight chain V region (clone 165.3m) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1071
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1071
A;Title: Both ight and igg anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1071
A;Accession: PH1071
A;Accession: purple: acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-91 cTIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;10-83/Domain: immunoglobulin homology < NMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glight chain V region (clone 17s.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH-1992
J. Exp. Med. 176, 761-779, 1992
A;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cA;Reference number: PH-1971; MUD:92381444; PMID:1512540
A;Reference number: PH-1970
A;Reference number: Aid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-96 <TIL>A;Experimental source: B cell, strain [NZB x NZW]F1
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
F;16-90/Domain: immunoglobulin homology <NMM>
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                                                                                                                                                                                                                                                                                                                   1 NIVMIQSPKSMSMSVGERVILSCKASENVGTYVSWYQQKSBQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                               1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RFAGSGSAADFSLTISSVHAEDLADYYCEQSYNYPWTFGGGTKLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                             Length 107;
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80.8%; Score 454; DB 2; Length 96;
Best Local Similarity 93.9%; Pred. No. 2.9e-33;
Matches 92; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTF 98
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                                                                                                                                                         Score 459; DB 2;
Pred. No. 1.2e-33;
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
                                                                                                                                                         81.7%;
82.2%;
                                                                                                                                                         Query Match
Best Local Similarity 82.2
Matches 88; Conservative
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Best Local Si
Matches 86;
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61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig Kappa chain V region - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: 32191
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32191
A;Accession: S32191
A;Accession: S32191
A;Accession: S32191
A;Accession: S32191
A;Accession: S32191
A;Cross-references: EMBL:X70095; NID:g288260; FIDN:CAA49700.1; PID:g288261
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM*>
Ig Kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42466
A;Status: preliminary
A;Accession: S42466
A;Status: preliminary
A;Accession: S42466
A;Status: preliminary
A;Besidues: 1-117 - SHI>
A;Crass-references: EMBL:X78108, NID:g460824; PIDN:CAA54998.1; PID:g460825
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 DIVMIQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHIGVPD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%; Score 429; DB 2; Length 117;
llarity 78.5%; Pred. No. 5.5e-31;
Conservative 10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.0%; Score 427; DB 2; Length 107; 78.5%; Pred. No. 7.6e-31;
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Matches 84; Conserv
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A,Accession: A90298
A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
A,Rosidues: 30-149 c&MI>
A,Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not
C,Comment: The mature chain has 12 additional residues at its amino end, due to a tan-
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light ()
Ain sulfide bonds: In some cases, such as 154 and 19M, the subunits associate into
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: duplication; heterotetramer; immunoglobulin homology
F)1-29/Domain: aignal sequence #status predicted <1G>
F)20-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F)21-131/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain precursor V region (WRL-RF28L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S04577
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
Submitted to the EMBL Data Library, March 1989
A;Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami: A;Reference number: S04577
A;Accession: S04577
                                                                                                                                                                                                                                                                                                                                                A Molecule type: mRNA
A Residues: 41-149 «RAB»
R Smith, G.P.
Biochem. J. 171, 337-347, 1978
A Filtle: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
A; Reference number: A90298; WIID: 78186617; PMID:418775
A;Accession: A90823
A;Molecule type: DNA
A;Residues: 1-71 <KEL>
A;Note: the sequence was determined from the differentiated gene
R;Rabbitts, T.H.; Hamlyn, P.H.; Matthyssens, G.; Roe, B.A.
Can. J. Blochem: 58, 176-187, 1980
A;Title: The variabllity, arrangement, and rearrangement of immunoglobulin genes.
A;Reference number: A90753; MUID:80176554; PMID:6245773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-127 < KOF>
A; Cross-references: EMBL:X14622; NID:G52400; PIDN:CAA32775.1; PID:G52401
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer: immunoglobulin
P;-20) Domain: signal sequence #status predicted <SIG>
F;21-127) Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.1%; Score 422; DB 1; Length 149; 78.5%; Pred. No. 2.9e-30; cive 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 127;
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illarity 75.7%; Pred. No. 4.5e-30;
Conservative 10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;64-129/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 78.5
Matches 84; Conservative
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Best Local Similarity
Matches 81; Conserv
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FQUADED Species: Mus musculus (house mouse)
C; Accession: 190265
C; Accession: PQ0265
R; Lohnan, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A; Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal
A; Reference number: PQ0265; MUID:92039046; PMID:1937027
A; Accession: PQ0265
A; Molecule type: mRNA
A; Residues: 1-119 < LOH;
A; Cross-references: GB:M59985
C; Comment: This protable region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: noomplementarity-determining 1
F; 62-68/Region: complementarity-determining 2
F; 101-109/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NIVMTOSPKSMSMSVGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
81 RFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYSSPWTFGGGTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 RFTGSGSGTDLTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.0%; Score 416; DB 2; Length 119; Best Local Similarity 77.6%; Pred. No. 7.8e-30; Matches 83; Conservative 8; Mismatches 16; Indels
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Search completed: August 16, 2004, 11:09:11 Job time : 11.5157 secs

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mus musculu mus musculu

homo sapien

homo sapien mus musculu

mus musculu mus musculu homo sapien

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                                          homo sapien
homo sapien
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-82059477; PubMed=6170937;
Hamlyn P.H., Gait M.J., Milstein C.;
Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxymucleoride method of RNA sequencing.";
Nucleic Acids Res. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 30-136.
MEDLINE=73053310; PubNed=4638343;
Svasti J., Milstein C.;
"The complete amino acid sequence of a mouse kappa light chain.";
Biochem. J. 128:427-444(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-V REGION MOPC 21. FRAMEWORK-1.
                                         PPO159
PPO159
PPO1669
PPO1668
PPO1619
PPO3977
PPO397
PPO397
PPO3977
PPO3977
PP
    P01622
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14902 MW; 8CDD85113996D1C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; V00810; CAA24192.1; ALT_TERM.
PIR; A93736; KVMS21.
PDB; 11GC; 03-UUN-95.
InterPro; 1PR007110; Ig-1ike.
InterPro; 1PR007596; Ig-v.
Pfan; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regIon; Signal; 3D-structure.
SIGNAL
CHAIN.
30 136 IG KAPPA CHAIN V-V R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig kappa chain V-V region MOPC 21 precursor.
                                                                                                                                                                                                                                                                   136 AA
                                                                                                                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 562;
KV35 MOUSE
KV26 HUMAN
KV16 HUMAN
KV16 HUMAN
KV17 HUMAN
KV31 MOUSE
KV37 MOUSE
KV37 MOUSE
KV35 MOUSE
KV30 MOUSE
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                                                                                                                                               US-09-889-300A-2
562
1 NIVMTQSPKSMSNSVGERVT......CGQGYSXPYTFGGGTKLEIK 107
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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KV1A HUMAN
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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P01632;
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                                                         30 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myelona MPC 11.";
Biochem. J. 171:337-347(1978).
Biochem. J. 171:337-347(1978).
-!- MISCELLANDOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL RESIDUE OF TYPICAL KAPPA CHAINS.
                                  1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                Gaps
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 41-149 FROM N.A.

BEDLINES BOUTSES 4. PubMed-6245773;

Rabbitts T.H. Hamlyn P.H., Matthyssens G., Roe B.A.;

"The variability, arrangement, and rearrangement of immunoglobulin
"The variability, arrangement, and rearrangement of immunoglobulin
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith G.P.; "Sequence of the full-length immunoglobulin kappa-chain of mouse
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o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-V REGION MPC11.
FRANEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRANEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                               90 RFTGSGSAIDFILIISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 136
                                                                                 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
7e-53;
0; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                149 AA
               0; Mismatches
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=78186617; PubMed=418775;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
      100.08;
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      d Similarity 100.
107; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
"Nucleic acid and protein sequences of phosphocholine-binding light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                               16434 MW; B0480C87B682AC3E CRC64;
                                                                                                                                                                                          , DB 1;
6.2e-38;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region S107A.
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Pred. No. 6
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InterPro; IPR003596; Ig_v.
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78.5%;
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                                  NIVMTQSPKSMSMSVGERVTLTCKASENV-----VTYVSWYQQKPEQSPKLLIYGASNR 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salomon A.;
Submitted (AUG-1996) to Swiss-Prot.
Submitted (AUG-1996) to Swiss-Prot.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                    YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:00069555; F:antigen binding; NAS.
GO; GO:00069555; F:antigen binding; NAS.
GO; GO:0006955; F:antigen binding; NAS.
InterPro; IPR003109; Ig_v.
SMART; SW00410; Ig_v.
SMART; SW00416; IGv. 1.
PROSITE; PSS0835; Ig_LIKE; 1.
PROSITE; PSS0835; Ig_LIKE; 1.
PROSITE; PSS0835; Ig_LIKE; 1.
PROMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
DOWAIN 41 55 FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneider M., Hilschmann N.;
"The primary structure of a monoclonic immunoglobulin-L-chain subgroup IV of the kappa type (Bence-Jones protein Len).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
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COMPLEMENTARITY-DETERMINING-3.
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65.5%; Pred. No. 6.4e-34;
tive 18; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                             21-UTL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
119 kappa chain V-IV region Len.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                 114 AA
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MEDLINE=76004342; PubMed=50995;
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PDB, 1EEU, 03.7EB-01.
PDB, 1EEU, 09.7EB-01.
PDB, 1EK3, 06.MAR-01.
PDB, 1LVE, 21.AN-98.
PDB, 3LVE, 18.MAX-99.
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Best Local Similarity
Matches 74; Conserv
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                                                                                                                                                                                                                                                                                                                           KV4A HUMAN
P01625;
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SEQUENCE
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                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE-86041884; FubMed=2997713;
MATSh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marsh P.;
Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14966 MW; 6413A22FD0738832 CRC64;
                                          01-JAN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-VUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-IV region Bl7 precursor.
Homo sapiens (Human)
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134 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 13:6531-6544(1985).
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SMART, SM00406, IGV; 1.
PROSTIE, PS50835, IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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ID KV1M_HUMAN
KV4C HUMAN
P06314;
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PRT;
                                                                    Biochemistry 33:14848-14857(1994)
                                                                                                                 MEDLINE=81267384; PubMed=6167731;
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1D KVIO HUMAN STANDARD; 1

C PO1607;

DT 21-JUL-1986 (Rel. 01, Created)
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68; Conservative
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Best Local Si
Matches 68,
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                                                                                                                                                                                                                                                      Scand. J. Immunol. 5:677-684 (1976).
-!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                         Capra J.D., Klapper D.G.; "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1g kappa chain V-I region WAT.
Edwaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=95086080; Pubmed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTFISSLQPEDIATXYCQQXNNWPPTFGQGTKVEVK 107
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 375; DB 1; Length 108; 65.4%; Pred. No. 4.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
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            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
19 kappa chain V-I region Lay.
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HSSP; P01667; IREI.
GO; GO:0005276; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                          SEQUENCE.
MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFEMI, PF00047; 19; 1.
SMAR; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN F
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88
108
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tes 70; Conserv
                                                                                                                             NCBI TaxID=9606;
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KVIY HUMAN
ID FRIGE;
P80362;
NOV-199F
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                                                                                                                                                                                                                                                             Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.; Panagiotopoulos protein Wat."; J. Mol. Biol. 147:185-193(1981).

T. Mol. Biol. 147:185-193(1981).

T. Mol. Biol. 147:185-193(1981).

R. MSCELLAMBOUS: This is a Bence-Jones protein.

R. GO, GO:0005576; C:extracellular; NAS.

GO; GO:0005555; P:antigen binding; NAS.

GO; GO:0005555; P:antigen binding; NAS.

R. GO; GO:0005555; P:antigen binding; NAS.

R. GO; GO:0005557; P:Rumune response; NAS.

R. R. GO; GO:0005576; Ig.-V.

R. Pfanis PF00047; Ig.-1.

R. PROSTE; PS50835; IG.LIKE; 1.

PROSTE; PS50835; IG.LIKE; 1.

PROSTE; PS50835; IG.LIKE; 1.
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Solomon A., Stevens F.J., Schiffer M.; Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers."
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FRAMEWORK-4.
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63.6%; Pred. No. 1.5e-32;
tive 20; Mismatches 19;
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TN -> SD (IN REF.
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KV1V_HUMAN
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                                                                                                             Palm W., Hilschmann N.;
"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=76039568; Pubmed=182131;
Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemiatry 14:4943-4925 (1975).
-- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                              Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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11902 MW; 9E8143E1188BCE2A CRC64;
                                                                                                                                                                                 combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975)
                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: This is a Bence-Jones protein.
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig kappa chain V-I region Rei.
                                                                                                                                                                                                                                                                                                                     PIR; A91663; KIHURE.
PDB; 1REI; 17-FEB-84.
PDB; 1ARZ; 12-NOV-97.
PDB; 1BWW; 29-DEC-99.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006555; F:antigen binding; NAS.
INCERPO: IPR00110; IG-1ke.
InterPro; IPR00110; IG-1ke.
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                                                                                                    MEDLINE=76023758; PubMed=809329;
                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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449
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                                    Homo sapiens (Human)
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108 AA;
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Length 108;

Score 365; DB 1; Pred. No. 5e-32;

64.9%;

Query Match Best Local Similarity

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Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   amyloid protein (BAN).";
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                                                                                                 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEI 106
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
20; Indels
                                                                                                                    11840 MW; CD3FD944FE96FD37 CRC64;
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01-07N-1988 (Rel. 06, Last sequence update)
15-0U1-1999 (Rel. 38, Last annotation update)
11g kappa chain V-IV region JI precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                               13.AUG-1987 (Rel. 05, Created)
13.AUG-1987 (Rel. 05, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-I region BAN.
                                                                                                                                                                                                                  108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Muller F.B., O'Connor T.P., Benson M.D.;
"Polymorphism in a kappa I primary (AL) amy,
Mol. Immunol. 23:73-78 (1986).
PRI, AOHOPS, HATUSN
HSSP, P80362; IWTL.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005576; F:antigen binding; NAS.
GO, GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
PROMAR; SM00406; IGV: 1.
PROSITE; PSSG835; IG_LIKE; 1.
Immunoglobulin V region; Amyloid.
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 19; Mismatches
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 67; Conservative
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Best Local Similarity
Matches 68; Conserv
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KV4B_HUMAN
ID KV4B_HUMAN
AC P06313;
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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                      HODDE-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: This is a Bence-Jones protein.
Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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Nature 276:785-790(1978).
-!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
HSSP; P01679; 2FBJ.
HNCPPRO; IPR007110; Ig-like.
InterPro; IPR003556; Ig_v.
Pfam; PP00047; ig; 1.
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MEDLINE=70073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 FRAMEWORK-1,
34 COMPLEMENTARITY-DETERMINING-
49 COMPLEMENTARITY-DETERMINING-
56 COMPLEMENTARITY-DETERMINING-
88 FRAMEWORK-3.
97 COMPLEMENTARITY-DETERMINING-
107 FRAMEWORK-4.
88 BY SIMILARITY.
11671 MW; C8D2A616ODBD0618 CRC64;
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Pred, No. 2.2e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Mismatches
                                                                                                                                                                                          PIR; A01868; KHHUHU.
HSSP, P80362; UWTL.
GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0006955; P:immune response; NAS.
Interpro; IPR007110; Ig-like.
Interpro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
PR0SITE; PS50835; IG, ILKE; 1.
PROSITE; PS50835; IG, ILKE; 1.
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                                                                                                                                                                        Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIP-TFGGGTKVEIK 132
                                                                                                                                                                                                   Zachau H.G., \fi "Subgroup IV of human immunoglobulin K light chains is encoded by
   , Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Hau.
Homo sapiens (Human).
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 13:6515-6529(1985).
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                                                                                                               SEQUENCE FROM N.A. MEDLINE=86041853; PubMed=2997712;
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Best Tocal Similarity
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         Eukaryota; Metazoa;
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133 AA;
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HSSP; P01607; IREI.
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129 AA;
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MEDLINE-85014148; PubMed-6091049;
KICHOECK H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCPI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                 57 GVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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FRAMEWORK-1.
COMPLEMENTARIIY-DETERMINIG-1.
                                                                                                                                                                                                                                                            63.9%; Score 359; DB 1; Length 111; 63.1%; Pred. No. 2.2e-31; ive 17; Mismatches 20; Indels
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COMPLEMENTARITY-DETERMINING-2.
                                                                                          FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                           COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                    COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                         12041 MW; D7DF0609303453CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Daudi precursor.
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                                                           FRAMEWORK-1
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GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0005823; P: antigen binding; NAS.
GO; GO: 0006955; P: immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
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SWART, SW00406; ig; 1.
PROSITE, PS50835; IGV; 1.
Immunoglobulin V region; Signal.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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339
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111 AA;
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Best Local Similarity
Matches 70; Conserv
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P04432;
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Bulitz M., Kley H.-P., Zeitler H.-J.;

Bulitz M., Kley H.-P., Zeitler H.-J.;

Bulitz M., Kley H.-P., Zeitler H.-J.;

sequence of the variable part of a human L-chain of the Kappa-type.";

HOPPE-Seyler's Z. Physiol. Chem. 360:725-734(1979).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-!- MISCELLANEOUS: This is a Bence-Jones protein.
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15-UUL-1996 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 18, Last annotation update)
16 kappa chain V-I region Kue.
17 kappa chain V-I region Kue.
18 kappa chain W-I region Kue.
19 kappa chain W-I region Kue.
19 kappa chain W-I region Kue.
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18 kappa chain W-I region Kue.
18 kappa chain W-I region Kue.
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19 kappa chain W-I region Kue.
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                                                                                                                                                                                                            63.9%; Score 359; DB 1; Length 129; 59.8%; Pred. No. 2.7e-31; iive 19; Mismatches 24; Indels
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COMPLEMENTARITY-DETERMINING-1.
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                          COMPLEMENTARITY-DETERMINING-3.
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56 COMPLEMENTARITY-DETERMINING-
88 COMPLEMENTARITY-DETERMINING-
107 FRAMEWORK-4.
107 FRAMEWORK-4.
108 BY SIMILARITY.
12127 MW, 906679ASD90E4E98 CRC64;
110 FRAMEWORK-3.
119 COMPLEMENTARITY-DETERMININ
129 FRAMEWORK-4.
110 BY SIMILARITY.
1129
114235 MW, CAF076BC75574C8 CRC64;
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61 RFSGSGSGTEFTLTINSLQPDDFATYYCQQYSRYPYTFGQGTKLDIK 107

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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTY----VSWYQQKPEQSPKLLIYGASNRYT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                         Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                     SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.7%; Score 358; DB 1; Length 111; Best Local Similarity 61.3%; Pred. No. 2.9e-31; Matches 68; Conservative 21; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                       12099 MW; EC46C9D259213BE4 CRC64;
                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 3741/TEPC 111.
                    111 AA
                    PRT;
                                                                                                                                                                     Nature 276:785-790(1978).
                   STANDARD;
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                  KV3H MOUSE
P01660;
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Search completed: August 16, 2004, 11:08:35 Job time : 7.67713 secs

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August 16, 2004, 11:08:06; Search time 31.6682 Seconds (without alignments) 1066.069 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_vertebrate:\*
sp\_unclassified:\*

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*

sp\_rvirus:\* sp\_bacteriap:\*

sp\_archeap:\*

					SUMMARIES	
Result		.* Query	.* Query			
No.	Score	Match	Length	99	di.	Description
н	406	72.2	108	11	QBVIJO	Q8vijo mus musculu
71	378	67.3	66	11	Q9JL74	Q91174 mus musculu
m	370.5	62.9	107	4	Q96SA9	Q96sa9 homo sapien
4	369	65.7	108	4	Q9UL77	
Ŋ	366.5	65.2	109	4	Q9UL78	Q9ul78 homo sapien
φ	366	65.1	107	11	Q9ERZ9	Q9erz9 mus musculu
7	363.5	64.7	109	4	Q9UL85	Q9u185 homo sapien
α	363,5	64.7	238	11	Q99M37	Q99m37 mus musculu
ወ	358	63.7	234	4	Q7Z473	Q7z473 homo sapien
10	357	63.5	108	4	Q9UL.79	Q9ul79 homo sapien
11	357	63.5	236	4	Q7Z3Y4	Q7z3y4 homo sapien
12	354	63.0	108	4	Q9UL70	
13	351.5	62.5	107	4	Q9UL81	
14	350.5	62.4	238	11	QBVCI6	Q8vci6 mus musculu
15	347.5	61.8	239	11	Q8VC55	Q8vc55 mus musculu
16	347	61.7	108	4	09UL83	Ogul83 homo sapien

Q7tmk3 mus musculu Q8k1f3 mus musculu Q920e9 mus musculu Q8k1f1 mus musculu Q7ts98 mus musculu		xeno mus mus	Oggyfo mus musculu Q96pf6 homo sapien Q95lA2 mus musculu Q7tqm2 mus musculu Q91ws9 mus musculu	chis omo mus omo mus	Q811c3 mus musculu Q7tmko mus musculu Q9n0w5 oryctolagus Q9u180 homo sapien Q8t0f8 mus musculu Q9j178 mus musculu
Q7TMK3 Q8K1F3 Q920E9 Q8K1F1 Q7TS98	Q9UL86 Q9R1A5 Q91WF8 Q8VDD0	Q7SZ36 Q811U6 Q920E6 Q8K1F2	Q9QYF0 Q96PF6 Q9JL82 Q7TQM2 Q91WS9	Q9U410 Q8NEKO Q8R062 Q8TCD0 Q8VCP0	Q811C3 Q7TMK0 Q9NOW5 Q9UL80 Q8K0F8
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## ALIGNMENTS

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STREALM-C3H/Hed-lpr/lpr,
MEDLINE=96409289; PubMed=8814271;
MEDLINE=96409289; PubMed=8814271;
MIOCH M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
MIOCH M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-hpr mice and lupus mice with nephritis.";
EME., U59155; AAB02917.1;
PR. A.33933; A.33933.
Interpro; IPR007110; Ig-like.
Interpro; IPR007110; Ig-like.
Fram, PP00047; ig, I.
SMART; SM00406; IGv; I.
SMART; PSS0835; IG_LIKE; I.
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                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA; 11859 NW; 68506D75613DBFBE CRC64;
                                           Q8VIJO;
01-MAR-2002 (TrEMBirel. 20, Created)
01-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Anti-DNA light chain (Fragment).
                                 108 AA
                                 PRT;
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL. ARZ06032; AARF69330.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
                                                                            61 RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107
                                    61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;
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1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                  Match 65.9%; Score 370.5; DB 4; Length 107; Local Similarity 65.4%; Pred. No. 1.8e-32; les 70; Conservative 19; Mismatches 17; Indels 1;
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SEQUENCE FROM N.A.
MUX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                             107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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EMBL, AF035037; AAD56273.1; -.
PIR, 849047; B49047.
PIR, 534063; S34083.
HSSP, POLGO7, IREL
InterPro, IPR007110; IG-like.
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PIR; B49047; B49047.

PIR; S34083; S34083.

PIR; S34086; S34083.

InterPro; IPR00710; Ig-like.

InterPro; IPR00710; Ig-v.

Pfan; PR0047; ig, I.

SMART; SM00406; IGv: I.

PROSTIE; PS50835; IG_LIKE; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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EMBL, AF035029, AAD56265.1; -. BR. D30609, DAD5.265.1; -. BRSP, PR038029, AAD56265.1; -. BRSP, PR03803, AMD5. InterPro; IPR07110; Ig-like. InterPro; IPR07110; Ig-like. InterPro; IPR073196; Ig-v. BR03896; Ig-v. BR03896; Ig-v. BR03896; Ig-v. BR03896; Ig-v. BR03896; Ig-v. BRART; SM00406; IGv; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.";
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           SOOCCOS
SOUDD BRANK REAR BREAR BRANK BRANK
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                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSERZ9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti human TNF-alpha light chain variable region (Fragment).
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                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fetus. 1, 2002111. Immunol. Immunopathol. 87:184-192 (1998).

EMBL, AP05108 A5 AAD56272.1; -. ETR, A30601, A30601.

PIR, A30601, A30601.

PIR, A30601, B30601.

PIR, B30601, B30601.

PIR, C30601, C30601.

PIR, C30601, C30601.

PIR, C30601, D30601.

PIR, D30601, D30601.

PIR, D30601, D30601.

PIR, P30601, D30601.

PIR, P30601.

PIR, P30601, D30601.

PIR, P30601, D30601.

PIR, P30601.

PIR, P30
                                                            109 AA
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                                                         PRT;
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NON TER 109 109
SEQUENCE 109 AN
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                                                         PRELIMINARY;
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                                                                                                                                                                                                                          Fragment)
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Q9UL78;
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RESULT 5
Q9UL78
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                                                                                                                                     SECUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
Choning and sequencing of the light chain fragment of variable region genes of an anti-hTNF-a monoclonal antibody.";
J. Cell. Mol. Immunol. 12:21-26(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MTQSPKSMSMSVGERVTLTCKASENVV------TYVSWYQQKPEQSPKLLIYGASNRYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAWYQKKPGQSPELLVYFASTRESG
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SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Chen P., Deng dequencing of the single-chain antibody gene of human TNP-alpha specific monoclonal antibody.";
Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Homo saptiens (Human).
Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF262/53, AAG23804.1; -.
R PDB; 2AP2; 24-NOV-99
R PDB; 4ACA; 24-JUL-02.
R InterPro: IPR007110; Ig-11ke.
R InterPro: IPR007110; Ig-11ke.
R PRAMT; SM00406; IgV; 1.
R SNART; SM00406; IGV; 1.
R PROSITE; PS50835; Ig_ ILKE; 1.
R PROSITE; PS50835; Ig_ ILKE; 1.
R NOW TER 107 107
S SEQÜENCE 107 AA; 11784 MW; 2B15EBA6604A26G3 CRC64;
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Ol-WAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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STTPOS

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Ronnetenn M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worlby D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevcherko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
K.Zywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPDR
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                                                                                                                                                                                                                                                                                                           Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                             107
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                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK
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63.7%; Score 358; DB 4; Length 234;
Best Local Similarity 61.3%; Pred. No. 1.1e-30;
Matches 65; Conservative 21; Mismatches 20; Indels
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Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056256; AAH56256.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25,
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Q9UL79;
01-MAY-2000 (TEMBLrel. 13,
01-MAY-2000 (TEMBLrel. 13,
01-OCT-2003 (TEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences.
                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                     20
                                                                                                      80
                                                                                                                                                                                                           Q72473
Q72473;
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Q7Z473
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                                                                                                                                                                                                                 2 IVNTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NIVMTQSPKSMSMSVGERVTLTCKASENVV----TYVSWYQQKPEQSPKLLIYGASNRY 55
                                                                                                                                                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                      64.7%; Score 363.5; DB 4; Length 109; 65.4%; Pred. No. 1.1e-31; ive 19; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                        62 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                    62 FSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%; Score 363.5; DB 11; Length 59.8%; Pred. No. 2.9e-31; tive 22; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -
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                                             109 109
109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
  PROSITE, PS50835; IG_LIKE; 1.
NON_TER 1 109 109
SEQUENCE 109 AA; 11761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 2.
SWART; SM00406; IGV; 1.
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                                                                                                                              65.4%;
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Best Local Similarity 59.8%
Matches 67; Conservative
                                                                                                           Query Match
Best Local Similarity 65.4<sup>†</sup>
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
238 AA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. Mus musculus (Mouse).
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PIR, B32248; A32248

PIR, C32248; C32248

PIR, F32230; F32530

PIR, PH1042; PH1042

PIR, PH1044; PH1044

PIR, S07455; S07455

PIR, S07455; S07455

PIR, S24501; S24501

PIR, S24535; S24535

PIR, S24536; S24536

PIR, S24536; S24536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
SEQUENCE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                              099M37;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9UL70;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 68; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young D.C.;
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Q9UL81
ID Q9UL8:
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    RAT REPRETED SO YEAR SO WELL S
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TISSUE Skeletal muscl
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                                                                             Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                MEDLINE-98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 357; DB 4; Length 108; 60.7%; Pred. No. 5.4e-31; trive 21; Mismatches 21; Indels
    Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA; 11787 MW; DB5845F19724FB4E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fetts.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBI, APD3505; AAD5671.1; -.
PIR; S23638; S23638.
HSSP, PO1607; IREI.
IncerPro; IPR007110; Ig-like.
InterPro; IPR0047; Ig; 1.
SMART; SM00406; IGy; 1.
PROSITE; PSS0835; IG_LIKE; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last anno
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Best Local Similarity
Matches 65; Conserval
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                                                                                                                                                                         Mammalia; Euther
NCBI_TaxID=9606;
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NON TER
SEQUENCE
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Homo sapiens (Human).
Bukaryota, Mezaca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIK 129
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                                                                                                                                                                              Query Match 63.5%; Score 357; DB 4; Length 236; Best Local Similarity 62.6%; Pred. No. 1.5e-30; Matches 67; Conservative 19; Mismatches 21; Indels
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 354; DB 4; Length 108; 63.6%; Pred. No. 1.1e-30; tive 16; Mismatches 23; Indels
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1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                               the EMBL/GenBank/DDBJ databases.
Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC005332; AAH05332.1; -. Hypothetical protein. SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
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EMBL; AP035044; AAD56280.1; -.
PIR; PH0863; PH0863.
InterPro; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig_v.
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TISSUE=Colon;
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Best Local 8
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Q8VC55
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 351.5; DB 4; Length 107; 61.7%; Pred, No. 2.1e-30; ive 20; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Colon;
TISSUE-Colon;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R PIR; A22248; A32248.
R PIR; A32933; A33933.
R PIR; B32248.
R PIR; B30577; B30577.
R PIR; B30577; B30577.
R PIR; B30577; B30577.
R PIR; B30594; B3248.
R PIR; B30594; B3248.
R PIR; B30594; B3248.
R PIR; C27887; C27887.
R PIR; C32248; C32248.
R PIR; C32804; C32248.
R PIR; C32804; C32248.
R PIR; D29804; C32288.
R PIR; D29804; C32288.
                             NON TER 1 107
NON TER 107 107
SEQÜENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.",

fetus.",

Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; AF035031; AAD56269.1; -.

HSSP; P01607; 1REI.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-v.

Pfam; PP00047; Ig; 1.

PROSITE; PSS0835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                            (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VCI6
Q8VCI6;
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1 NIVMIQSPKSMSMSVGERVILICKASENVV-----TYVSWYQQKPEQSPKLLIYGASNRY 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
E BMBL; BCO21781; AAH21781.1; -.
E PRE, A3393; A3393; A3393.
E PRE, A3393; A3393.
E PRE, A3393; A3933.
E PRE, A3393; A3933; E PRE, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMARY, SW00406, IGV, 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS0290; IG MHC; 1.
HYPOTHELICAL protain.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
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l Similarity 58.9
66; Conservative
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us-09-889-300a-2.rspt

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Search completed: August 16, 2004, 11:10:29 Job time : 31.6682 secs

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Seguence

Sequence 167, App Sequence 167, App Sequence 53, Appl Sequence 53, Appl Sequence 167, App Sequence 167, App Sequence 167, App Sequence 167, App Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 167, Appl

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1 QVQLQQSGAELVRPGTSVXVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 554.5; DB 1; Length 119;
Pred. No. 5.4e-45;
3; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tso, J. Yun

APPLICANT: Tso, J. Yun

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: GPIB/IIA

NUMBER OF SQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
US-08-487-200-3
US-08-488-1208-14
US-08-488-1208-14
US-08-477-484B-167
US-08-107-689D-53
US-08-472-788A-85
US-08-472-788A-85
US-08-482-360-167
US-08-082-842A-85
US-08-136-389-167
US-09-136-389-167
US-09-136-389-167
US-09-610-888-167
US-09-610-888-167
US-09-610-888-167
US-09-610-888-167
US-09-610-888-167
US-09-610-888-167
US-09-610-888-167
US-08-428-257A-74
                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/ABENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
                                                                                                                                                                                                                                                                      Sequence 11, Application US/08458516
Patent No. 5777085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 91.6%;
Matches 109; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
3Y: linear
  USA
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                    RESULT 1
US-08-458-516-11
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                                                                                                                                          1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116
                                                                            August 16, 2004, 11:08:07 ; Search time 15.0852 Seconds
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Sequence 1(
Sequence 2)
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(GGDZ 6/ptodata/2/iaa/5A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/5A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS CCMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS CCMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-58-939-1
US-08-58-939-1
US-08-458-516-22
US-08-458-516-22
US-08-458-516-23
US-08-75-128-20
US-08-75-128-20
US-08-75-128-20
US-08-75-128-20
US-08-75-128-20
US-08-75-128-20
US-08-954-39
US-08-954-39
US-08-954-39
US-08-95-312-15
US-08-97-312-15
US-08-97-312-15
US-08-58-28
US-08-397-411-11
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US-08-477-728-14
US-08-474-040-3
US-08-474-040-14
                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-05262-9
US-08-656-586-4
                                                                                                                                                                                                389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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                                                        - protein search, using sw model
                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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Match Length DB
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Perfect score:
                                                                                                                                                                Scoring table:
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478.5
478.5
                                                        OM protein
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Maximum DB
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61 NEKFKGKATLIVUDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWPAYWGRGTLVTVSA 119
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                                                                                          61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: William M. Smith STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: DATE COMPATIBLE

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,516

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/059,159

FILING DATE: 03-MAY-1993

ATTORNEY AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 11823-37-3

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08767128 Patent No. 6111079
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APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSYALDO
APPLICANT: MURRAY, PETER JOSEPH
                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08458516
Patent No. 5777085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
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Best Local Similarity 91.6
Matches 109; Conservative
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US-08-767-128-10
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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLHWIGVINPGSGGTNY 60
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Э
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: ULCLOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.0%; Score 546.5; DB 3; Leng:h
Best Local Similarity 89.9%; Pred. No. 3e-44;
Matches 107; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-UN1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UN-1995
ATTOCNEY/AGENT INFORMATION:
NAME: CATTER, Charles G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8648.49USF1
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-589-939-1; Sequence 1, Application US/08589939; Patent No. 6015662; Patent ThrowarION; APPLICANT: Hackett, Jr., John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648
TELECONMUNICATION INFORMATION:
TELEPHONE: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                    USA
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CURRENT APPLICATION DATA

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61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.0%; Score 503.5; DB 1; Length 119; 80.7%; Pred. No. 3.3e-40; tive 12; Mismatches 8; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Co, Man Sung
APPLICANT: Tso, J Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/458,516
                    FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET UNDER: 11823-37-3
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELEPHONE: 415-326-2400
      APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-458-516-22
; Sequence 22, Application US/08458516
; Patent No. 5777085
                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 80.78
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-326-2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 NEKFKGRATLTADKSSTAYMOLTSLTSDDSAVYFCARTIVTTDYFDYWGQGTPLTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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Pred. No. 8.5e-41;
5; Mismatches 10; Indels
APPLICANT: OSECOW, DAVIG H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND TITLE OF INVENTION: COTROLS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,939
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPRENCE/DOCKET NUMBER: 5865.US.01
TELEPHONE: 847-935-1729
                                                                                                                                                                                                                   COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.9%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 138 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                  61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%; Score 503.5; DB 1; Length 449; 80.7%; Pred. No. 1.4e-39; ive 12; Mismatches 8; Indels 3;
                                                                                                                                                                         APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
GITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,4e-39;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159

FILING DATE: 03-MAY-1993
ATTORNEY/AEDYI TRFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET NUMBER: 11823-37-3
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: RIDAPY disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                         ; Sequence 13, Application US/08458516; Patent No. 5777085; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 449 amino acids
TYPE: amino acid
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Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
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                                                                                                                                                           US-08-458-516-13
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                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGSSVKVSCRASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY
                                                                                                                                                                                                                                                                       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                                                                                                                                              DB 1; Length 222;
                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
APPLICANT: TSo, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                            82.0%; Score 503.5; DB 1.
80.7%; Pred. No. 6.4e-40;
tive 12; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION ...
FILING DATE:
CLASSIPICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03.MAY.1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISSTRATION NUMBER: 30,23
REFRENCE/DOCKET NUMBER: 30,23
REFRENCE/DOCKET NUMBER: 11823-37-7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11823-37-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                   LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 amino acids
                                                                                                                                                                         Query Match
Best Local Similarity 80.77
Matches 96; Conservative
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Best Local Similarity 80.74
Matches 96; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                         , MOLECULE TYPE: protein US-08-458-516-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Market P
CITY: San Francisco
STATE: California
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US-08-458-516-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-458-516-23
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                                                                                                                                                                           61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                              61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGW?AYWGQCTLVTVSS 119
                                                      1 OVOLOQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGL3WIGVINPGSGGTNY
Gaps
                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-157-370-2
US-09-157-370-2
Sequence 2, Application US/09157370A
Patent No. 6262238
GENERAL INFORMATION:
APPLICANT: STEIFE, Boris
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072
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3; Gaps

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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFRGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR----DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NEKFKGKATFTADTSSNTAYMQVSSLTSEDSAVYYCARIYYGHLWFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQQSGVELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
79.9%; Score 490.5; DB 3; Length 119;
Best Local Similarity 78.2%; Pred. No. 5.4e-39;
Matches 93; Conservative 10; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INVORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Paurick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STREET: 755 Page Mill Road
CITY: 94304-1018
COMUTERY: USA
AIDE ADA OF THE FORM:
MEDIUM TRYE: 1EM PC compatible
COMPUTER READABLE FORM:
MEDIUM TRYE: 1EM PC compatible
COMPUTER: 1EM 
                      8648,49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-881-037-65; Sequence 65, Application US/08881037; Patent No. 6080588; GENERAL INFORMATION:
                                                       TELECOMMUNICATION INFORMATION TELEPHONE: 612/371-5278 TELEFAX: 612/332-9081 TELEFAX:
                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-767-128-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NEKFKGKATLTRDKSSSTAYLQLSSLTSEDSAVYYCARGGYYYFDYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-767-128-20
Sequence 20, Application US/08767128
SEPERAL INFORMATION:
APPLICANT: UCPEZ, OSYALDO
APPLICANT: GCEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: USA DINCEOSTIDES CODING THEREFORE
NUMBER OF SEQUENCES:
SADDRESSEE: MARCHARL, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St CITY: Minneapolis
STREET: NN
COUNTRY: USA
ZIP: FFACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.0%; Score 497.5; DB 3; Length 117; 80.3%; Pred. No. 1.2e-39; ive 11; Mismatches 11; Indels 1
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER PELING DATE: 1997-07-06
EARLIER PELING DATE: 1995-07-06
EARLIER PELING DATE: 1999-07-06
EARLIER PILING DATE: 1999-07-06
SOFTWARE: PELING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTX: USA
ZIP: 55402
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTERO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/09258
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION 1424
PRIOR APPLICATION 04-05-1996
FILING DATE: 05-JUN-1996
PRIOR APPLICATION NUMBER: 05-JUN-1996
PRIOR APPLICATION NUMBER: 05-JUN-1996
PRIOR APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
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APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UTW-1995
ATTORNEY/AGENT INFORMATION:
NAME: CARTER, Charles G.
REGISTRATION NUMBER: 35,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.3 Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus sp.
US-09-157-370-2
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61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARD------($PWFAYWGQGTLVTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAELVKPGASVKLSCKASGYTFSSYWMEWVKQRPGQVL3WIGEINPGNGHTNY 60
  1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGL3WIGVINPGSGGTNY 60
                                                                                61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPW7AYWGQGTLVTVSA 116
                                                                                                           61 NEKFKSKATLIVUKSSSTAYMQLSSLTSEDSAVYYCARSFTTARGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLHWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.5%; Score 482; DB 2; Length 122; 72.1%; Pred. No. 3.5e-38; Live 19; Mismatches 9; Inde.s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC comparible
COMPUTER: IBM PC comparible
COPERATING SYSTEM: PC C-DOS/MS-DOS
SOFTWARE: WORD PERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: U1y 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U2/07/916,09843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,949
TELEPHONE: (312) 715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: ALLEGRETTI & WITCOFF, LTD.
10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAN: (312) 715-1000
TELEPAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 amino acids
amino acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSET
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 88; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 10 SOUTH
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
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US-07-916-098A-10
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                                                                                                                                                                                                                                  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-----PWFAYWGQGTLVTVS 115
                                                                                                                                                                                        1 QVQLLESGAELARPGASVKLSCKASGYTFTSYGISWVKQRTGQGLEWIGEIYPRSGNTYY 60
                                                                                                                                               1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08737560A
Patent No. 5928893
GENERAL INFORMATION:
APPLICANT: KANG, Chang-Yuil
APPLICANT: KIM, Joong-Gon
ITILE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
ITILE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
ADDRESSEE: KANG, Chang-Yuil
STREET: Rang, Chang-Yuil
STREET: Rang, Chang-Yuil
STREET: Rang, Chang-Yuil
STREET: Chang-Yuil
STREET: Chang-Yuil
STREET: Chang-Yuil
STREET: Chang-Yuil
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                                                              DB 3; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.6%; Score 482.5; DB 2; Length 119; ilarity 79.0%; Pred. No. 3e-38; Conservative 8; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCUNTRY: Republic of Korea
ZIP: 151-057
ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 4B4-1-1 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Regublic of Korea
COUNTRY: Regublic of Korea
TIP: 135-110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,560A
FILING DATE: 13-NOV-1996
CLASSIFICATION: 536
                                                            79.1%; Score 485.5; DB 3
80.0%; Pred. No. 1.6e-38;
cive 4; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: RR 95-8176
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                        Query Match
Best Local Similarity 80.0°
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 94; Conserva
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US-08-737-560A-10
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; TOPOLOGY:
US-08-881-037-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQPGAELVKPGASVKLSCKASGYTFSSYWMHWVKQRPGQVLEWIGEINPGNGHTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NEKFKSKATLIVUKSSSTAYMQLSSLISEDSAVYYCARSFITARAFAYWGQGTLVIVSA 119
                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: HONG, Hyo Jeong
APPLICANT: HONG, Hyo Jeong
APPLICANT: HONG, Hyo Jeong
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yuil
APPLICANT: KANG, Chang-Yuil
APPLICANT: Young Jun
APPLICANT: WANG, Chang-Yuil
APPLICANT: WANG, WANG
TITLE OF INVENTION: HYMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: HYMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: HARMACEUTICAL COMPOSITION COMPRISING SAME
FILE REFERRING: 1399-11-12
CURRENT FILING DATE: 1999-11-12
SOFTWARE: PACHLIN Ver. 2.1
SEQ ID NO 39
LENGTH: 119
TYPE: PRT
TYPE: PRT
CREATURE:
CREATURE:
CREATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Variable OTHER INFORMATION: region of heavy chain of mouse monoclonal antibody OTHER INFORMATION: 4B4-1-1 US-09-438-954-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%; Score 481.5; DB 4; Length 119; 79.0%; Pred. No. 3.8e-38; tive 8; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2. Application US/08392419;
Patent No. 5624659
GENERAL INFORMATION:
APPLICANT: Bigner, Darell D.
TITLE OF INVENTION: METHOD OF TREATMENT:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,827
FILING DATE: 19-MAR-1993
                                                                                                                                                                            Sequence 39, Application US/09438954
Patent No. 6458934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.0
Matches 94; Conservative
SA 116
                                 |:
121 SS 122
                                                                                                                          RESULT 14
US-09-438-954-39
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August 16, 2004, 11:10:36 ; Search time 42:1345 Seconds (without alignments) 864.269 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NBW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NBW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_NBW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_NBW_PUB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Description	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Segmence
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DB	12	12	16	16	16	16	16	16	16	13	12	12	16	19	16
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% Query Match	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	84.5	82.0	82.0	82.0	82.0	82.0
Score	554.5	554.5	554.5	554.5	554.5	554.5	554.5	554.5	554.5	519	503.5	503.5	503.5	503.5	503.5
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-10-410-997-5	10-411-0	-10-287-994-5	-10-410-913-5	-10-411-037-5	-10-411-026-5	-10-410-962-5	-10-411-049-5	-10-410-930-5	-10-410-997-5	-10-411-012-5	-10-287-994-5	10-410-913-5	-10-307-276B-	-10-006-773-1	-10-435-614-1	-435-614-2	-10-435-614-1	-10-435-614-2	-10-307-276B-	-10-307-276B	0-447-257-	-10-010-729	-10-467-546-	-10-467-546-	-10-153-024-	-10 - 360 - 053	-10 - 360 - 05	0-307-276B	-10-460-59
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## ALIGNMENTS

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USC-10-411-037-54

IGS-10-411-037-54

Sequence 54, Application US/10411037

Publication NO US20040043446A1

Sequence 54, Application US/10411037

Publication NO US20040043446A1

APPLICANT: Neeser Technologies, Inc.

APPLICANT: Neeser Technologies, Inc.

APPLICANT: Sove Shawn

APPLICANT: Bowe Caryn

APPLICANT: Bowe Caryn

TITLE OF INVENTION: ALACTOSIDASE A

FILE REFERENCE: 04083-01-502

CURRENT FILING DATE: 2003-044,092

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR PILING DATE: 2003-044,692

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR PILING DATE: 2003-06-07

PRIOR PELICATION NUMBER: US 60/391,777

PRIOR PELICATION NUMBER: US 60/404,249

PRIOR PELICATION NUMBER: US 60/404,249

PRIOR PELICATION NUMBER: US 60/407,527

PRIOR PELICATION NUMBER: US 60/407,527

PRIOR PELICATION NUMBER: US 60/407,527

NUMBER OF SEQ ID NOS: 75

SOFTWARE PERCENTING

PRIOR PELICATION NUMBER: US 60/407,527

NUMBER OF SEQ ID NOS: 75

SEQ ID NO 54

LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-10-411-037-54
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APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, X.
APPLICANT: Bowe, Caryn
ITILE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYJOCONJUGATION OF INTERFERO
ITILE OF INVENTION: ALPHA;
FILE REFERENCE: 040853-01-5055
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PILING DATE: 2001-10-19
PRIOR PELLING DATE: 2001-10-19
PRIOR PELLING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-07-17
PRIOR PELLING DATE: 2002-07-17
PRIOR PELLING DATE: 2002-07-17
PRIOR PELLING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
                 APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Carn
APPLICANT: Bowe, Carn
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REFERENCE: 04003-04-09
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54, Application US/10411049 Publication No. US20040082026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
Bayer, Robert
Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Mus musculus
US-10-410-962-54
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US-10-411-049-54
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| Publication No US20040063911A1 |
| GENERAL INCPRANTION: |
| APPLICANT: Neose Technologies, Inc. |
| APPLICANT: DeFrees, Shawn |
| APPLICANT: DeFrees, Shawn |
| APPLICANT: Bayer, Robert |
| APPLICANT: Chen, Xi |
| TITLE OF INVENTION: NEWTYION: NEWTHODS AND PROTEINS/PEFTIDES PRODUCED BY THE |
| TITLE OF INVENTION: METHODS |
| FILE REFERENCE: 040853-01-5053 |
| CURRENT APPLICATION NUMBER: US 60/328,523 |
| PRIOR APPLICATION NUMBER: US 60/344,692 |
| PRIOR PLING DATE: 2002-06-25 |
| PRIOR PELING DATE: 2002-06-25 |
| PRIOR PELING DATE: 2002-06-25 |
| PRIOR APPLICATION NUMBER: US 60/391,777 |
| PRIOR APPLICATION NUMBER: US 60/391,777 |
| PRIOR APPLICATION NUMBER: US 60/404,249 |
| PRIOR APPLICATION NUMBER: US 60/407,527 |
| PRIOR PLING DATE: 2002-08-16 |
| PRIOR PRIOR PLING DATE: 2002-08-16 |
| PRIOR PRIOR DATE: 2002-08-16 |
| PRIOR
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                                                                                                                    Gaps
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                                      Length 119;
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                                                                                                                    4; Indels
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                                      DB 12;
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                                  Query Match
90.3%; Score 554.5; DB 17
Best Local Similarity 91.6%; Pred. No. 1.8e-45;
Matches 109; Conservative 3; Mismatches 4
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91.6%; Pred. No. 1.8e-45;
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Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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Matches 109; Conservative
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4; Indels
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Pred. No. 1.8e-45;
3; Mismatches 4;
                                                                                                                           Sequence 54, Application US/10410997; Publication No. US20040126836A1, GENERAL INFORMATION. APPLICANT: Neose Technologies, Inc., APPLICANT: DeFrees, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 54, Application US/10411012
Publication No. US20040132640A1
GENERAL INFORMATION:
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Best Local Similarity 91.6<sup>3</sup>
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Mus musculus
US-10-410-997-54
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US-10-411-012-54
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Accordance to the control of the control
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                                                                                                                                                                                                                                                                                                                                                         Length 119;
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Best Local Similarity 91.6%; Pred. No. 1.8e-45;
Matches 109; Conservative 3; Mismatches 4
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 54
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54, Application US/10410930 Publication No. US20040115168A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT;
CORGANISM: Mus musculus
US-10-410-930-54
                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                     US-10-411-049-54
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APPLICANT: DeFrees, Slawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Chan, Xi
APPLICANT: Bowe, Caryn
APPLICANT: Defree
APPLICANT: Defree
APPLICANT: Color-10-10
APPLICANT: Col APPLICANT: Neces Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE FILLE OF INVENTION: METHODS
FILE REFERENCE: 040853-01-5051
CURRENT APPLICATION NUMBER: US/10/411,012
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10 9 9 61 NEKFKGKATLIYUDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119 61 NEKFKGKATLITADKSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116 1 QVQLQQSGABLVGPGTSVRVSCKASGYAFINYLIEWVKQRPGQGLEWIGVIYPGSGGTINY 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY Gaps 3, DB 16; Length 119;

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Matches 109; Conservative
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APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
APPLICANTON: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-00
CURRENT FILING DATE: 2002-11-05
PRIOR PILING DATE: 2001-10-19
PRIOR PAPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
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            PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-06-25
PRIOR PRILOR TOWNWBER: US 60/396,594
PRIOR PELLING DATE: 2002-00-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN VERSION 3.2
SEGTWARE: PATENTIN VERSION 3.2
PRIOR APPLICATION NUMBER: US 60/344,692
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Publication No. US20040137557A1
GENERAL INFORMATION:
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91.6%;
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-012-54
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; ORGANISM: Mus musculus
US-10-287-994-54
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Best Local Similarity
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US-10-287-994-54
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer Robert
APPLICANT: Bayer Robert
APPLICANT: Bayer Robert
APPLICANT: Bayer Robert
APPLICANT: Hake, David
APPLICANT: Hake, David
APPLICANT: Chen, Xi
APPLICANTON: GIYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5081
CURRENT FILING DATE: 200-04-09
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PALICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-25
PRIOR PELING DATE: 2002-06-25
PRIOR PELING DATE: 2002-06-28
PRIOR PELING DATE: 2002-0
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Sequence 8, Application US/20020173035A1
GENERAL INFORMATION:
APPLICANT: YUHAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
FILE REFERENCE: CV17440
CURRENT APPLICATION NUMBER: US/10/146,305
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3; Gaps
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4; Indels
3; Mismatches
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Publication No. US20040142856A1
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Best Local Similarity 91.65
Matches 109; Conservative
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CORGANISM: Mus musculus
US-10-410-913-54
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GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Ghon, XI
TILE OF INVENTION: RATHODS
TITLE OF INVENTION: RATHODS
TITLE OF INVENTION: WHERE: US/10/411,026
CURRENT APPLICATION NUMBER: US 60/328,523
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PRIOR DATE: 2002-06-07
PRIOR PRIOR DATE: 2002-06-07
PRIOR PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PRIOR DATE: 2002-07-17
PRIOR DAT
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Publication No. US2004007783641

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
TILLE OF INVENTION: GENAULOCYTE COLONY STIMULATING FACTOR: REWODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REFERENCE: 040853-01-5054
1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60
                                                                               61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                     61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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82.0%; Score 503.5; DB 12;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; 1
                                                                                                                                                                                                                                                                                                                                                     ; Sequence 53, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
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US-10-410-962-53
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Sequence 53, Application US/10411037

Publication No. US20040043446A1

Sequence 53, Application US/10411037

Publication No. US20040043446A1

APPLICANT: Degree: Renormalian APPLICANT: Degree: Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Caryn
TITLE OF INVINTION: ALACTOSIDASE A. REMODELING AND GLYCCCONJUGATION OF ALPHA
TITLE OF INVINTION: ALACTOSIDASE A.
TITLE OF INVINTION: ALACTOSIDASE
TITLE REFERENCE: 040823-04-09

PRIOR FILING DATE: 2001-10-10
PRIOR PELING DATE: 2001-10-10
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR PELING PERIOR PER
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 519; DB 13; Length 138;
Pred. No. 5.3e-42;
5; Mismatches 9; Indels
            ; CURRENT FILING DATE: 2002-05-15
; PRIOR PAPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO
; LENGTH: 138
; TYPE: RT
; CREANIEN: Escherichia coli
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Best Local Similarity 83.6%;
Matches 102; Conservative
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121 SS 122
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                                                                                                                                           DB 16; Length 119;
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                                                                                                                                      Query Match 82.0%; Score 503.5; DB 10
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8
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82.0%; Score 503.5; DB 16
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8;
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US-10-410-930-53
US-10-410-930-53
, Sequence 53, Application US/10410930
; Publication No. US20040115168A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                        ; ORGANISM: Homo sapiens
US-10-411-049-53
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US-10-410-930-53
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APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Experiment to Experiment TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA: BOOK 1-0.1-0.0
PRIOR PELICATION NUMBER: US 60/328,523
PRIOR PELICATION NUMBER: US 60/391,777
PRIOR PELING DATE: ZOO2-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PLING DATE: ZOO2-08-16
PRIOR PLING DATE: ZOO2-08-16
PRIOR PLING DATE: ZOO2-08-16
PRIOR FILING DATE: ZOO2-08-16
PRIOR FILING DATE: ZOO2-08-16
NUMBER OF SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NO S:
LENGTH DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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80.7%; Pred. No. 1.4e-40;
tive 12; Mismatches 8
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2003-04-09
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-15
PRIOR PLING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SECTIMENT VERFILING VERFION 3.2
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Sequence 53, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.7
Matches 96; Conservative
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ORGANISM: Homo sapiens
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GenCore version 5.1.6
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August 16, 2004, 11:08:06; Search time 12.4843 Seconds (without alignments) 893.780 Million cell updates/sec US-09-889-300A-1 614 1 QVQLQQSGAELVRPGTSVKV......ARDGPWFAYWGQGTLVTVSA 116 OM protein - protein search, using sw model Title: Perfect score: Sequence: Run on:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Id heavy chain V r	g heavy	g heavy	q heavy chain pr	17-6 antibody he	q heavy chain v	g gamma-	g heavy chain	g heavy chain v	ש	g heavy chain V	q qamma chain -	g gamma-2a chain	g heavy chain V	g heavy	g heavy chain v	g heavy chain pr	chain	g heavy chain pr	g heavy chain	g heavy chain V	b	g heavy chain V	g heavy chain	g heavy chain v	g heavy chain pr	q heavy chain v-	ntibody Fab Jel	g heavý chain
SUMMARIES	ID		260067																A27472		г.	A54378	48	PL0231	57	S)	VMSG'	9660	853751	4867
	DB	2	7	7	8	7	~	Н	7	7	7	7	7	7	0	~	7	7	Ŋ	7	Н	7	7	71	0	7	Н	N	7	N
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	Score		52	491.5	9	•	7.	œ	œ	œ	m'	83.	82	82.	÷	48	•	478	477.5	7	475.5	7	ω.	472.5	-		٩.	9	9	
	Result No.		2	m	4	ß	9	7	ω	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2

School
19 heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragment 19 heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragment C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence\_revision 10-Oct-1997 #text\_change 23-Mar-2001
C;Date: 23-Feb-1996 #sequence\_revision 10-Oct-1997 #text\_change 23-Mar-2001
C;Date: 23-Feb-1996 #sequence\_revision 10-Oct-1997 #text\_change 23-Mar-2001
R;Mien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, P.; Crainic, R.; Hogl: Nat. Structure of the complex between the fab fragment of a neutralizing antibody fracession: 860067; MUID:95292109; PMID:7539711
A;Accession: 860067
A;Molecule type: mRNA
A;Residues: 1-123 <WIES
A;Residues: 1-123 <WIES
A;Cross-references: EMBL: R84698; NID:9773225
R;Wien, M.W.; Hogle, J.M.

heavy chain	heavy chain	heavy chain	heavy chain	pelB leader/Ig hea	heavy chain	heavy chain	heavy chain	chain	chain	chain		heavy chain	heavy	heavy chain	chain
A30502	825176	MHMS18	A39276	PC4402	PL0232	819969	538717	B22769	566537	F48677	E32513	A56700	S55542	\$37201	G28195
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	75.9	75.9						75.7		75.5		75.3	75.3	74.9	

## ALIGNMENTS

C;Keywords: h F;15-98/Domai Query Match Best Local Matches 10	C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin P; 15-98 Domain: immunoglobulin homology < IMM*> Query Match: immunoglobulin homology < IMM*> Query Match 87.2%; Score 535.5; DB 2; Length 123; Best Local Similarity 87.8%; Pred. No. 1.5e-41; Matches 108; Conservative 1; Mismatches 7; Indels 7; Gaps 2;  Matches 108; Conservative 1; Mismatches 7; Indels 7; Gaps 2;  Qy
Db	1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRLGQDLEWIGVINPGSGGTNY 60
ο ν	61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWQQGTLVT 113
pp qa	61 NEKFKGKATLIJADKSSSTAYMQLSSLTSDDSAVYFCARSSPYDYDGYWYFDVWGAGTTVT 120
Qy 11	114 VSA 116
	<u></u> ;
UD 12	121 VSS 123

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Gaps ; 9

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UC2269
UC2269: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 Regenence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: JC2269; PC2186
R;Kurome, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasumoto, M.; Ka
J; Biochem: 115, 608-614, 1954
A;Title: Expression of recombinant mouse/human chimeric antibody specific to human GM
A;Reference number: JC2269; MUID:94334310; PMID:7520038
A;Molecule type: mRNA
A;Residues: 1-117 KUR>
A;Accession: JC2289
A;Molecule type: protein
A;Residues: 2-27 KUZ>
A;Experimental source: hybridoma cell
C;Comment: This protein is specific to human P-selectin.
C;Comment: This protein is specific to humanoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin homology cIMM>
F;2-98/Domain: immunoglobulin homology cIMM>
F;99-106/Region: J segment
F;107-117/Region: J segment
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(230562
Ig heavy chain V region (27.7.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996.
C;Accession: (230562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, T. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen A;Reference number: A30562; MUDD:89110066; PMID:2464031
A;Accession: (230562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 cSIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPGSSSTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLQQSGAELTKPGASVNMSCKASGYTFTSYWMHWVKQRPGQGLEWIGYINPGTAYTEH 60
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                                                                                                                                1 QVQLQQSGAELVRPGTSVXVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                 80 NEKFKSKATLITUDISSSTAYMQLSSLISDDSAVYYCARLVGGFAYWGQGTLVIVSA 135
                                                                                                                                                                                                                                                             61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
         Length 135;
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                                                                           Indels
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                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
             Score 491; DB 2;
Pred. No. 1.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.4%; Score 487.5; DB 279.0%; Pred. No. 3.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.4%; Score 487.5; DB 278.6%; Pred. No. 3.1e-37; ive 10; Mismatches 14
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                           96; Conservative
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nes 94; Conserv
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92; Conserv
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Best Local S:
Matches 92
                   Query Match
Best Local S
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C;Date: 06-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C;Date: 06-Bis, 1985
J;Rofler, R; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof
J. Exp. Med. 161, 805-815, 1985
J;Reference number: A30577; MulD:85159423; PMID:3920343
A;Reference number: A30577; MulD:85159423; PMID:3920343
A;Residues: 1-135 ckOF>
A;Cross-references: GB:M37621
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  July chain V region - mouse

If heavy chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Species: Worlew ansculus (house mouse)
C; Accession: 520640; 250644
ERILOSMAIN, F. FRAY, T. M.; Novick, K. E., Monestier, M.
Stlosmain, M.; FRAY, T. M.; Novick, K. E., Monestier, M.
Submitted to the EMBL Data Library, February 1992
A; Reference number: 820639
A; Reference number: 820639
A; Accession: 820640
A; Status preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Coss_references: EMBL:X65002; NID:G52600; PIDN:CAA46135.1; PID:G52601; EMBL:X64999; N
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NANFKGKATLTADKSSSIVYMQLSSLTSDDSAVYFCARDFYDYDVGFDYWGQCTTLTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubmitted to the Brookhaven Protein Data Bank, January 1995.
Reference number: A52979; PDB.IFPT
Contents annotation; X-ray cryptallography, 3.0 angstroms, residues 1-123; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin; pyroglutamic acid; 15-54/Domain: immunoglobulin homology alMMS; il/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted; ;22-96/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                                                                                                                                                                                                                                                                     Length 123;
                                                                                                                                                                                                                                                                                                 Score 526; DB 2; Length 12.
Pred. No. 1.1e-40;
5; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.0%;
Matches 102; Conservative
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Best Local Similarity 77.33
Matches 92; Conservative
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9 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY Gaps 3; 13; Indels

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igheavy chain precursor V region (A003 40/5G7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: F29380
C;Accession: F29380
C;Accession: F29380
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable A;Reference number: A92612; MUID:88007582; PMID:3115981
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                                                      F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;281-350/Domain: immunoglobulin homology <IM3>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;154-220.288-348,394-4527/Disulfide bonds: #status predicted
F;247_250.253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EVQLQQSGPELVNPGASVKASCKASGYTFITVVAHWVKQKPGQGLEWIGYINPNKDGTKF 79
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C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C;Accession: C30566
C;Accession: C30566
B;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of n
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A;Accession: C30560
A;Retus: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-118 <MAX-
A;Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 487; DB 1; Length 474; 77.1%; Pred. No. 1.5e-36; Live 11; Mismatches 14; Indels
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Pred. No. 6.1e-37;
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F;157-222/Domain: immunoglobulin homology <IM1>
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Best Local Similarity
Matches 94; Conserv
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A, Molecule type: mRNA
A, Residues: 1-137 <CHE>
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A,Residues: 138-172, 'P',174-189,'FP',193-376,'T',378-474 <TU2>
A,Molecule type: DNA
A,Residues: 138-172, 'P',174-189,'FP',193-376,'T',378-474 <TU2>
R,Ollo, R.; Rougeon, P.
Nature 296, 761-763, 1982
A,Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma, Reference number: A26233
A,Molecule type: DNA
A,Coession: A26233
A,Molecule type: DNA
A,Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A,Cors-references: GB:000461
A,Residues: 138-161,'L',Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
A,Coession: A353-12350, 1994
A,Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A,Reference number: A53598, MUD:94216359; PMID:7512967
A,Reference number: A53598, MUD:94216359; PMID:7512967
A,Residues: 234-251 <KIM>CGOmment: The a allele sequence is shown.
C,Genetics:
A,Introns: 138/1; 236/1; 258/1; 368/1
C,Complex: An immunoglobulin heteroteteramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C,Superfamily: immunoglobulin C region; immunoglobulin heterotetramer; immunoglobulin C region; immunoglobulin C regio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gramma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: 11-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S25057; A02157; A26235; A26232; A26233; A353598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific A;Reference number: S25057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:X67210, NID:g54826, PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleoride sequence of immunoglobulin gamma2b chain gene cloned from A;Reference number: A02157; MUID:80120716; PMID:6766534
     61 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARHYYGSSSFAYWGQGTLVTVSA 119
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A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murin
A;Reference number: A26232; MUID:80081502; PMID:117549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĕ
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A; Residues: 138-161, L., 163-189, FP', 193-474 < YAM>
A; Residues: 138-161, D00461
A; Cross-references: GB:J00461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A; Title: Structure of the constant and 3' untranslated regions and a structure of the constant and a structure of the constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: $25057
A, Status: preliminary
A, Molecule type: .mRNA
A, Residues: 1-474 <FIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Contents: a allele
A;Accession: A02157
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1g gamma chain - mouse

C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Nus musculus (house mouse)
C.Species: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C.Accession: S38950
B.K.Rebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
Biol. Chem. Hoppe-Seyler 34', 993-1000, 1993
A.Title: Primary structure of the murine monoclonal IggZa antibody mAb735 against alp A;Reference number: S38950; MUID:94128242; PMID:8297501
A.Reference number: S38950
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-246 < KLE
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riklebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgGza antibody mAb735 again: A;Reference number: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                       NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARNYGSSYGLAYWQQGTLVTVSA 138
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C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aymolecule type: protein
AyResidues: 1-446 «KLE>
C;Genetics: 1
Aymap position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
E;1-446/Product: Ig gamma-2a chain #status experimental «MAT>
E;1.117/Domain: V-D-J region «VDJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA
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File 214/Domain: C1 region <CHR>
File 214/Domain: C1 region <CHR>
File 214/Domain: C2 region <CH2>
File 214/Domain: C2 region <CH2>
File 214/Domain: C3 region <CH3>
File 1446/Domain: C3 region <CH3>
File 1446/Domain: G3 region <CH3>
File 1446/Domain: Maunoglobulin homology <IMM>
File 1446/Domain: immunoglobulin homology <IMM>
File 1446/Domain: immunoglobulin homology <IMM>
File 1446/Domain: main immunoglobulin homology <IMM>
File 1446/Domain: main immunoglobulin homology <IMM>
File 1446/Domain: main immunoglobulin homology <IMM>
File 1446/Domain: minerchain #status predicted
File 247,227,229/Disulfide bonds: interchain #status predicted
File 247/Binding site: carbohydrate (Asn) (covalent) #status experimental
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79.5%; Pred. No. 1.9e-36;
tive 7; Mismatches 16
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Best Local Similarity 79.53
Matches 93; Conservative
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Matches
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C;Species: Wus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: 821810
R;Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A;Pescription: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chancestiption: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chancestiption: S1810
A;Reference number: S21810
A;Reference number: S21810
A;Residues: 1-138 cOST-
A;Residues: 1-138 cOST-
A;Cross-references: EMBL:X56936; NID:954163; PIDN:CAA40257.1; PID:954164
C;Genetics: 15/3
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology < IMM>
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R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the BMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s Na;Reference number: $3859
A;Reference number: $3859
A;Reference number: $3859
A;Reference number: $13859
A;Retaus: preliminary
A;Molecula type: mRNA
A;Residues: 1-118 <mn.
A;Residues: 1-118 <mn.
A;Residues: 1-118 <mn.
A;Residues: I-118 <mn.
A;Residues: I-18 <mn.
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                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLITADKSSSTAYMQLSSLISDDSAVYFCAR--DGFWFAYWGQGTLVTVSA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 heavy chain V region (ASWV1) - mouse (fragment)
Species: Mus musculus (house mouse)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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                                                                                Gaps
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       Length 118;
78.8%; Score 484; DB 2; Length 11 78.0%; Pred. No. 6.4e-37; ive 10; Mismatches 14; Indels
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79.8%; Pred. No. 8.4e
:ive 7; Mismatches
                                                                            92; Conservative
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Best Local Similarity 79.8
Matches 95, Conservative
Query Match
Best Local Similarity
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80 NEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYCAREGPAGDYWGQGTTLIVSS 135
                                                                                                          completed: August 16, 2004, 11:09:11
ne : 13.4843 secs
                                                                                                              Search co
              임
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R. Sikder, S. K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
T. Immunol. 142, 888-893, 1989
A. Tittle: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bit A, Reference number: A30562; MUD:89110066; PMID:2464031
A. Reference number: A30562, MUD:89110066; PMID:2464031
A. Accession: B30562
A. Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-119 < cstra
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer; immunoglobulin homology < INM>
F;15-98/Domain: immunoglobulin homology < INM>
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R;Kaartinen, M.; Rocca Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0076
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                     E30562
Ig heavy chain V region (27.10.2) - mouse (fragment)
Ig heavy chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Date: 23-Mar-1989
                                                                                                              61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
                                                                                                                                                      61 NEKFKGKATLITVDTSSSTAYMQLSSLTSEDSAVYFCARGKFAMDYWGQGTSVTVSS 117
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A; Residues: 1-141 < KAA>
A; Residues: 1-141 < KAA>
A; Crose-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
A; Crose-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted < SIG>
F; 20-141/Product: Ignal sequence #status predicted < MAT>
F; 34-117/Domain: immunoglobulin homology < IMM>
F; 50-54/Region: complementarity-determining 2
F; 123-125/Region: U2 segment
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A Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
A Tucker P.W.;
Tullegitimate recombination generates a class switch from C mu to C
T "Illegitimate recombination generates a class switch from C mu to C
T delta in an IgD-secreting plasmacytoma.";
PPTS, A02033; HVMS77.
R HSSP, P01810; 2F8J.
R InterPro; IPRO7110; Ig-like.
R InterPro; IPRO7110; Ig-like.
R InterPro; IPRO7110; Ig-like.
R InterPro; IPRO7110; Ig-like.
R RNSAT; SM00407; ig; I.
SMRAT; SM00406; IG_V.
R PROSITE; PS50835; IG_LIKE; I.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse)
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BY SIMILARITY
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                                                                             HV42 MOUSE
HV39 MOUSE
HV30 MOUSE
HV16 MOUSE
HV3K HUMAN
HV33 MOUSE
HV31 MOUSE
                                                                                                                                                                                                                                                                             HV3B HUMAN
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138 AA;
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Best Local Similarity
Matches 92; Conserv
  HV48 MOUSE
P03980;
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HV48 MOUSE
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                                                                                                                                                                              August 16, 2004, 11:08:06; Search time 8.32287 Seconds (without alignments) 725.728 Million cell updates/sec
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1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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HV31 HUMAN
HV32 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
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                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                              "The generic Dasis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Bur. J. Immunol. 12:1023-1032[1982].

-!- MISCELLANEOUS: FROM MAULES 1982 THE SIZES OF SEVERAL OTHER

DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 heavy chain V region 93G? precursor.
Mus musculus (Mouse).
Eukaary cas Metaacoa (Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Mus. Mus.
                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.8%; Score 471.5; DB 1; Length 120; 76.7%; Pred. No. 1.4e-42; ive 8; Mismatches 15; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A/J;
MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                           SEGMENT, JH2.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP, P01789; IMCP.
InterPro; IPR07110; Ig-like.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin heavy Chain.";
Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=81131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 36-65.
120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1. ...
SMART; SMO406; IGV; 1. SPROFITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
STANDARD;
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120 AA;
                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=10090;
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 HV03 MOUSE
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HV02_MOUSE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYDFDYWGQGTPLTVS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD----GPW-FAYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                            1 OVOLOOSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKORPGOGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                        76.5%; Score 469.5; DB 1; Length 140; 76.9%; Pred. No. 2.7e-42;
                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION 93G7.
IG-LIKE.
                                                                                                                                                                                                                                                                                                         15514 MW; 25A4CBBE31DASCE8 CRC64;
                                                                                  EMBL, J00493; AAA38128.1; -.
PIR, A94264; HVMSG7.
HSSP, PO1810, 2FBJ.
HSSP, PO1810, 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Ffan; PF0047; ig; 1.
PROSITE; PSS0835; IGv; 1.
Immunoglobulin V region; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 A.A.
                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J00529; AAA38170.1; -.
                                                                                                                                                                                                                                                                                                                                                                              93; Conservative
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139
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PDB; 1A6U; 27-MAY-98.
                                                                                                                                                                                                                                                                                         140 AA;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                  61 NEKFKGKATLTADKSSSTAYMQLSSLTŞDDSAVYFCAR----DGPWFAYWGQGTLVTVŞA 116
                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981)
-:- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOWA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                             20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYMMFWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                                                                                                              1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                         IG HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                      FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                       75.9%; Score 466; DB 1; Length 139; 74.2%; Pred. No. 6.3e-42; ive 11; Mismatches 16; Indels
                                                                                                                                                              COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
                                                                                                                                                                                                                                              15419 MW; 1B57DD4FD0C9F465 CRC64;
PDB; 1A6W; 15-JUL-98.
InterPro; IRRO07110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGv.
IRRUPOSTER; PS50835; IG LIKE; 1.
IRRUNOGlobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region S43 precursor.
                                                                                                                                                                                                     JH2 SEGMENT.
BY SIMILARITY.
                                                                                                                                                    FRAMEWORK-2
                                                                                                                                                                                           D SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, PO1810, 2FBJ.
InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig_v.
Pfam, PF00C47, ig, 1.
SMART, SM00406, IGv; 1.
PROSITE, PS50835, IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J00539; AAA38172.1; -.
PIR; A02038; G2MS43.
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                              139 AA;
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLQQSGPELVKPGASVKASCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                              1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                    20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWNQRPGRGLEWIGRIDPNSGGTTY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE-83076344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
                                                                                                                                                                                                                                                                                                         2
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BY SIMILARITY,
N-LINKED (GLCNAC. .,) (COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.2%; Score 455.5; DB 1; Length 117; llarity 73.5%; Pred. No. 6.5e-41; Conservative 14; Mismatches 16; Indels 1
                                                                         COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                  Length 137;
                                                                                                            COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- MICCELLANDOUS: THIS PROTEIN BLYINGLY.
-:- SIMILARITY: CONCAINS I immunoglobulin-like domain.
-:- SIMILARITY: CONCAINS I immunoglobulin-like domain.
R PIR; A02039; MMS4E.
R HSSP; P01789; MCP.
R InterPro; IPR00710; Ig-1ike.
R InterPro; IPR003596; Ig-v.
R Ffam; PPP00447; ig-v.
R Pfam; PPP00447; ig-v.
R PROSITE; PS50835; IG LIKE; I.
V Immunoglobulin V region; Glycoprotein.
                                    CHAIN V REGION S43
                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 117
117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                             15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                74.4%; Score 457; DB 1; 73.7%; Pred. No. 5.5e-41; ive 12; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-GCT-2003 (Rel. 42, Last annotation update)
Igh heavy chain V region MOPC 104E.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA
                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                   FRAMEWORK-3.
                                                                                                                                                                      SEGMENT
                                  IG HEAVY CH
FRAMEWORK-1
                                                                                                                                                   D SEGMENT
                                                                                                                                                                                                                                                                                      Local Similarity 73.7
Les 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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137
137 AA;
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86; Conserv
mmunoglobulin
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Matches 86
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Res. 8:3591-3601(1980)

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Nucleic Acids
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P06329;
                                 REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                   61 NOKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTIVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLTADKSSSTAYMOLSSLTSDDSAVYFCARDGFW-FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKGKATLIVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117
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MANY OF
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 01, Last nonotation update)
10-CCT-2003 (Rel. 42, Last nonotation update)
1g heavy chain V region MPC 11.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                       Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=81053741; PubMed=6253904; Zakut R., Cohen J., Givol D.; "Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPCII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                    Trearrangements in heavy chain V-region generates to the segments.";

Nature 283:35-40(1980).

- INSCELLANBOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTBINS THAT BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, WANN HICH OCCUR IN THE D AND J SEGMENTS.

- INSCELLANBOUS: THIS PROTEIN BINDS DEXTRAN.

- INSCELLANBOUS: THIS PROTEIN BINDS DEXTRAN.

- INSCELLANBOUS: THIS PROTEIN BINDS DEXTRAN.

R RSCEL242; MHMSJS.

R INTERPRO; IPRO0356; 19-V.

R RICHEPRO; IPRO0356; 19-V.

R PFan; PRO0406; 109: 1.

R SMART; SMO0406; 109: 1.

R PROSITE; PSS0835; 15 LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 454.5; DB 1; Length 117; 73.5%; Pred. No. 8.3e-41; tive 14; Mismatches 16; Indels 1:
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117 117
117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region U558.
Mus musculus (Mouse).
                                                                                                                    117 AA
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BY SIMILARITY.
                                                                                                                    PRT;
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SEQUENCE.
MEDLINE=80078170; PubMed=6765983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 73,5
Matches 86; Conservative
                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                HV13 MOUSE
P01757;
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61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR----DGPWFAYWGQGTLVTVS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=64182519; PubMed=6201362;
Dildforp R., Bovens V., Slekevitz M., Beyreuther K., Rajewsky K.;
Dildforp R., Bovens V., Slekevitz M., Beyreuther K., Rajewsky K.;
A V region determinant (idiotope) expressed at high frequency in B
1ymphocytes is encoded by a large set of antibody structural genes.";
EMBO V 3:517-523(1984).
PIR, A02037; MHMS15.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
11-JUN-1999 (Rel. 38, Last annotation update)
15-JUN-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 15.3.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                            74.0%; Score 454.5; DB 1; Length 121; 71.9%; Pred. No. 8.7e-41; ive 11; Mismatches 18; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
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120 J SEGMENT.
96 BY SIMILARITY.
120
13311 MW, 914453F426F09834 CRC64;
                                                                                                                                                                                                                                                                                                        121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 432; DB 1;
Pred. No. 2e-38;
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; l.
SWART; SW00406; IGv; l.
PR05TE; PS50835; IG_LIKE; l.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.48;
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 71.9
hes 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
106
22
120
120 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OVOLOOSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGLEWIGWIYPGDGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   HEAVY CHAIN V REGION VH558 A1/A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                 SEQUENCE FROM N.A. MEDIME=2509340; PubMed=2578321; Yancopoulos G.D., Alt F.W.; Yancopoulos G.D., Alt F.W.; "Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION VH558 .
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NEKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 427; DB 1;
Pred. No. 6.4e-38;
neavy chain V region VH558 Al/A4 precursor.musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                      EMBL; M3787; AAA38499.1; --
PIR; A02029; HVMSA1.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
Imminoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.5%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                        Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
82; Conserv
                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV51 MOUSE
P06330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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HV51 MOUSE
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                                                                                   NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGP-WFAYWGQGTLVTVSA 116
                                                                                                 61 NEKFKSKATLIVDKSSSATYMQLSTPISEDSAVYCARWDYEGDRYFDVWGTGTTVIVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                          Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
cell 24:625-637(1981).
--- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELAXED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWWHWVKQRPGQGLEWIGNINPGNGGTNY
                             1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                      1 QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWMHWIRQRPGQGLEWIGGINPSNGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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  13; Mismatches 20; Indels
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81.6%; Pred. No. 3.9e-38;
iive 7; Mismatches 11;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
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SMART; SM00406; IGv; 1.
FROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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nes 80; Conservative
 83; Conservative
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117 AA;
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                                                                                                                                                                                                                                                                     Mus musculus
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01-JAN-1988
15-JUL-1999
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P01748;
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HV52_MOUSE
ID HV52 MC
AC P06327;
DT 01-JAN-
DT 15-JUL-
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P06327;
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61 NEKFKGKATLTADKSSTAYMOLSSLTSDDSAVYFCAR 98
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79.6%; Pred. No. 1.5e-36;
iive 8; Mismatches 12;
                                                                                     62 EKFKGKATLTADKSSSTAYMOLSSLTSDDSAVYFCA
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P01749;
21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
21-UTL-1986 (Rel. 01, Last annotation update)
Ig heavy chain V region 3 precursor.
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Les 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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81.2%; Pred. No. 1.5e-36;
ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                             69.2%; Score 425; DB 1; Length 118; 68.6%; Pred. No. 1e-37; ive 14; Mismatches 21; Indels
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COMPLEMENTARITY-DETERMINING-1.
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118 118
118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
119 heavy chain V region 102 precursor.
Mus musculus (Mouse).
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J SEGMENT.
BY SIMILARITY.
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PIR, A02040; MHMS38.
HSSP; P01789; 1MCP.
INCEPPC; IPR007110; Ig-like.
INCEPPC; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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Best Local Similarity 81.2
Matches 78; Conservative
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Best Local Similarity
Lass 81; Conserve
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117 AA;
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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";

"Call 24:825-637 (1931).

"Call 24:825-637 (1931).

"IN SCELLANDOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

"RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES."

"RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES."

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"RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES."

"RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES."

"RELATED GENES THAT COULD ENCODE V REGION 186-1."

"A SIGNAL CHAIN V REGION 186-1."

"THE CHAIN CHAIN CHAIN V REGION 186-1."
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                                                       21 VQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHPSDSDTNYN 80
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2 VOLOQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYN 61
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV09_MOUSE STANDARD; PRT; 117 AA.
P01753; P11271;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                              Baltimore D.,
"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.",
Cell 24:625-637(1981),
-!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBOLIES.
                                                                                                                                                                               MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                           Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1.
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79.6%; Pred. No. 3e-36;
.ive 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION 3.
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MGD, MG196486, IGH-VJ558.
InterPro; IPR007110; IG-like.
InterPro; IPR003596, IG-V.
Ffam, PP00047, ig; 1.
SMART; SM00406, IGV; 1.
PROSITE; PS50835; IGLIKE; 1.
Immunoglobulin V region; Signal.
Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Best Local Similarity 79.0%
Best Local Similarity 79.0%
T8; Conservative
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                                                                                                                             SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

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Gaps

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80 NQKFKDKATLIVDKSSSTAYMQLSSLISEDSAVYYCAR 117

Search completed: August 16, 2004, 11:08:35 Job time : 8.32287 secs

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OM protein - protein search, using sw model	
Run on: August 16, 2004, 11:08:06; Search time 34.3318 Seconds (without alignments) 1066.069 Million cell updates/sec	
Title: US-09-889-300A-1 Perfect score: 614 Sequence: 1 QVQLQQSGAELVRPGTSVKVARDGPWFAYWGQGTLVTVSA 116	
Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5	
Searched: 1017041 seqs, 315518202 residues	
Total number of hits satisfying chosen parameters: 1017041	
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : SPTREMBL_25:*  1: sp_archea:* 2: sp_bacteria:* 3: sp_fung:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:* 10: sp_plant:* 11: sp_vresprent:* 11: sp_vresprent:* 12: sp_vresprent:* 13: sp_vresprent:* 14: sp_unclassified:* 15: sp_urins:* 16: sp_bacteriap:* 17: sp_archeap:* 17: sp_archeap:*	RESTORNED DE D

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Q924r5 mus musculu
SUMMARIES ID	090814 0971WT6 0934Q1 091WT1 091WT1 081WT1 081WT1 0824P7 0924P8 0924P8 0924R3 0924R3	Q924R5
DB		=
.% Query Match Length DB	4 6 1 4 1 4 4 4 1 6 1 1 1 1 1 1 1 1 1 1	139
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Score	0.44     4       0.000     6       0.44     0.44       0.04     0.04       0.00     0.00	463
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17	462.5	δ.	146	11	Q924R8	Q924r8	mus	musculu
18	62		œ	11	Q8K0Z4		gnw	mnscnjn
6	462	Ŋ.	4	11	Q924R0	Q924r0	mus	musculu
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23	460		4	11	Q924Q5	092495	mus	musculu
24	460	4.	4	11	Q91V67	091067	នការ	musculu
25	460	4.	4	11	Q924Q9		mus	musculu
56	458.5	4.		11	Q9QXF0		mus	musculu
27	58	4.	4	11	Q924Q3		mus	musculu
28	45	4.	~	11	Q921K1		mus	musculu
53	457.5	4.	4	11	Q924R2		EUM.	musculu
30	457	4.	-	11	Q9Z1C4		mus	musculu
31	457	4.	4	11	Q924R4		gnw	musculu
32	456	74.3	$\omega$	11	Q8VCV5		mus	musculu
33	453.5	ω.	-	11	O9QXE9		Buns	musculu
34	53.		4	11	Q924P5		mus	musculu
35	5	ω.	~	11	Q99L25		mns	musculu
36	ß	ω.	4	11	Q924R7		mus	musculu
37	449		0	11	Q9JL75		mus	musculu
38	4	ω.	4	11	Q924P9		mus	musculu
			N	11	Q920E8		mns	musculu
40	447		4	11	Q91VA2		mus	musculu
41	46.		9	11	Q8VDC9		mus	musculu
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45	c)	71.3	143	11	Q924P6		mus	musculu

## ALIGNMENTS

PRT; 473 AA.  Created) Last sequence update) Last annotation update) ; Craniata; Vertebrata; Euteleostomi;		Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schridl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carminci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Lyons P., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Rings B., Ringwald M., Rodriguz I., Sakamoto N., Sasaki H., Sato K., Schoenbadh C., Saya T., Shibata Y., Storch KF., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshawa-Boris A., Yoshida K., Hasegawa Y., Rawaji H., Kohtsuki S., "Functional annotation of a full-length mouse cDNA collection."; Phr.; S26746; S26746; S26746.
1 1 209BL4 PRELIMINARY; 01-JUN-2001 (TEMBLEE). 17, C. 01-JUN-2001 (TEMBLEE). 17, L. 01-OCT-2003 (TEMBLEE). 25, L. 01-OCT-2003	M N.A. /6J, TISSUE=: 5660; PubMed: inagawa A.V. kawa A., Nisl azaki Y., Go. arsuki Y., Go. w., Gaasterli	Kuehl P., Lewis S., Matsuo Schriml L.M., Staubli F., Sakai K., Okido T., Furuno Blake J., Boffelli D., Boju Brake J., Boffelli D., Boju Brownstein M.J., Hill D., Hoffelli D., Hoffelli D., Ma Wordone P., Ring B., Ringwa Sasaki H., Sato K., Schoenb Wynshaw-Boris A., Yoshida K Hayashizaki Y., Turucional annotation of a Wature 409:685-690(2001).  ENBL, AKOO7918; BAR25349.1).
LT 1  09DBL4  09DBL4; 01-JUN-2001 (TEEMBLRE) 01-JUN-2001 (TEEMBLRE) 01-CT-2003 (TEEMBLRE) 181006009R1k protein, 1GH-1 OR 1810060009R1K. Mus musculus (Mouse), Eukaryota; Metazoa; Cho Mammalia; Butheria; Rod NCB1_TAXID=10090;	[1] SEQUENCE FROW N.A. STRAIN=C57BL/6J, TISSUE=Pancreas; NWEDLINE=21085660; Pubmed=11217851; Kawai J., Shinagawa A., Shibata K., Arakawa T., Hara A., Fukunishi Y., Aizawa K., Izawa M., Nishi K., Kiyos Saito T., Okazaki Y., Gojobori T., Kadota K., Matsuda H.A., Ashburner N. Fleischmann W., Gaasterland T., Giss	Kuehl P., Lewis S., Mars Schrind L.M., Staubli F. Sakai K., Okido T., Furl Blake V., Boffelli D., E Brownstein M.J., Bult C. Gustinsich S., Hill D., Lyons P., Marchionni L., Lyons P., Marchionni L., Lyons P., Ring B., Ring Saki H., Sato K., Schrösaki H., Toyo-oka K., Suzuki H., Toyo-oka K., Shorshawaharis A., Yoshic Hayashizaki Y., Functional annotation C. Functional annotation C. Mature 409:685-690(2001) EMBL, AKOO718, BAB2534
RESULT 100908114 10000 1	RR RR RA RA RA RA RA RA RA RA RA RA RA R	# # # # # # # # # # # # # # # # # # #

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KRAIN-C57BL/GNCT; TISSUE=Hematopoietic Stem Cell;

KRAIN-C57BL/GNCT; PubMed=12477932;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Modin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

RA Richards S.W., Modernan N.A., Sacria M.M., Gay L.J., Hulyk S.M.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesiley W., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M. M., Madan J.W., Schwultz J., Nyers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Tignerstion and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                Score 526.5; DB 11; Length
Pred. No. 2.5e-46;
5; Mismatches 10; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053409; AAH53409.1; -...
                          MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50839; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Last annotation update)
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1 QVQLQQSGABLURPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                20 QVQLQQSGPELVXPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRVYFGDGDTNY 79
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QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLJEWVKQRPGQGLEWIGVINPGSGGTNY 60
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
V23-D-J-C MU
V23-D-J-C MU
Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069913; BAB63929.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
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01-JJN-2001 (TrEMBLrel. 17, Created)
01-JJN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 AA
                                                                                                                                                                                                                                                                                                                                        142 AA
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PIR, F28833, F28833.
PIR, PH1156, PH1156,
INTEMPRO, IPRO07110, Ig-like.
InterPro, IPR007110, Ig-like.
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00047, ig, 1.
SMART, SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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481 AA

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PRELIMINARY;
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Q8K172
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                                                                                                                                                                                                                                                                                                                                           80 SEKFKGKATLITIDKSSTAYMHLSSLITSEDSAVYFCARSSYYSYDLFAYWGQGTLVTVSA 139
                                                                                                                                                                                                                                                                                   20 QVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRTGQGLEWVGEIYPGSGNTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGP--WFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEKFKSKATLIVDKPSSTAYMQLSSITSEDSAVYYCAPDSNHLYFDYWGQGTTLIVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLJEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                          4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CSTBL/6;

STRAIN=CSTBL/6;

Cozono Y., Kozono H., Azuma T.;

Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ABG69915; BAB639311;

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-v.

Pfan; PR00047; ig: 1.

SMART; SM0046; IGv: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.4%; Score 475; DB 11; Length 143; 78.0%; Pred. No. 1.3e-41; ive 8; Mismatches 16; Indels
                                                                                                                                                                                                         ch 77.7%; Score 477; DB 11; Length 463; 1 Similarity 77.5%; Pred. No. 3.5e-41; 93; Conservative 7; Mismatches 16; Indels
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC003435; AAH03435.1; -. PIR; B45837; B45837.
                                                              MGD; MGI:96446; Igh-4.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 3.
SWART; SM00406; IGV.
PROSITE; PS00289; IG_MHC; 1.
PROSITE; PS002809; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; RAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
V165-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                            143 AA
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Best Local Similarity 78.0°
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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RESULT Q91WT1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWQQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRPGQGLVWIGWIYPGDGNTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus McBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%; Score 472.5; DB 11; Length 481; 77.8%; Pred. No. 1.1e-40; Live 6; Mismatches 19; Indels 1;
                                                                                                                                                                                                               TISSUE-colon;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Stubmitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig-W.
Fran, PF00047; ig-W.
SWART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
                                                     Last sequence update)
Last annotation update)
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                                      Created)
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PRT;
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Submitted (APR-2002) to the EN ENEL; BC028249; AAH28249.1; -
PIR, F33932; F33932.
PIR, PH1105; PH1105.
PIR, PH1104; PH1114.
PIR, PH1114; PH1114.
PIR, PH1119; PH1119.
PIR, PH1119; PH1125.
PIR, PH1125; PH1126.
PIR, PH1125; PH1126.
PIR, PH1131; PH1131.
PIR, PH1131; PH1131.
PIR, PH1131; PH1131.
PIR, PH1131; PH1131.
PIR, PH1131; PH1134.
PIR, PH1142; PH1142.
PIR, PH1142; PH1142.
PIR, PH1142; PH1143.
PIR, PH1142; PH1143.
                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                 Q91WT1;
01-DEC-2001 (TrEMBLrel, 19,
01-DEC-2001 (TrEMBLrel, 19,
01-OCT-2003 (TrEMBLrel, 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                       Hypothetical protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Breast tumor;
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145 AA;
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SEQUENCE
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Best Local &
                                                 Q924P7
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    RESULT 9
Q924P7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 NEKFKDKATLIADKSSTTVYMDLSRLISEDSAVYFCARHEDRGNYDGSLAWFVYWGQGTL 139
                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEKFKSKATLIYUDKPSSTAYMQLSSLISEDSAVYYCTREGDYDAMDYWGQGTSVIVSS 137
                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                Length 482;
PIR; PH1152; PH1152.

PIR; PH1153; PH1153.

InterPro: IPR007103597; Ig_cl.

InterPro: IPR003596; Ig_WC.

InterPro: IPR003596; Ig_WC.

InterPro: IPR003596; Ig_WC.

InterPro: IPR00407; Igf. 4.

SMART; SM00407; Igf. 4.

SMART; SM00406; IGV; 1.

PROSITE; PS02939; IG_MRC; 2.

PROSITE; PS02939; IG_MRC; 2.

SEQUENCE 482 AA; $\frac{5}{2}$121 MW; A06FP0835771D084 CRC64;
                                                                                                                                                                                                                                                                                                                                          15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC018322, AAH18322.1;
MGJ; MGI:96486, 1gh-V0558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           76.7%; Score 471; DB 11; 76.3%; Pred. No. 1.6e-40; cive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 AA.
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QUCX4;
01-MAR-2002 (TrEMBLrel. 20, C;
01-MAR-2002 (TrEMBLrel. 20, L;
01-OCT-2003 (TrEMBLrel. 25, L;
Hypothetical protein.
IGH-VJ558 OR AI893585.
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PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 2.
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.33
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 72.8
Matches 91, Conservative
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Q8VCX4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP)."; Submitted (AJG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB069918; BAB63934.1;
                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
WH186.2-D-J-C mu protein (Fragment).
Whs musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 4.3e-41;
9; Mismatches 14; Indels
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Last annotation update)
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PRT;
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PIR, F33932, F33932, PIR, PH1105, PH1106, PIR, PH1126, PH1126, PH1126, PH1126, PH1126, PH1137, PH1137, PH1137, PH1137, PH1137, PH1137, PH1137, PH1137, PH1150, PH1150, PH1150, PH1150, PH1151, PIR, PH1151, PH11
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01-MAR-2002 (TrEMBLrel. 20, C:
01-MAR-2002 (TrEMBLrel. 20, Lid
01-OCT-2003 (TrEMBLrel. 25, Lid
Hypothetical protein.
IGH-6. Mus musculus (Mouse).
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PROSITE; PS50835; IG_LIKE; 1.
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1 Similarity 77.5%;
93; Conservative
PRELIMINARY;
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Interpro, IPR007110; Ig-like.
Interpro, IPR003596; Ig_v.
Pfam, PF00047; ig, 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                        NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                          Q924P8;
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Q924R3
ID Q924R
AC Q924R
DT 01-DE
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                                                                                                                                                                                                                                            1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                          61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD-GPW-FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                        80 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARRLGRWYFDVWGAGTTVTVSS 137
                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067796; BAB63281.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                   Length 613;
                       TISSUE-Salivary gland;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC018315; AAH18315.1; -.
R MDJ; MGT:96448; Igh-6.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003306; Ig-Mrc.
R InterPro; IPR003306; Ig-Wr.
R PROSITE; PS00290; IG LIKE; 5.
R PROSITE; PS00290; IG-MHC; 3.
R PROSITE; PS00290; IG-MHC; 3.
R HYPOtherical procein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                         15; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                76.2%; Score 468; DB 11; 77.1%; Pred. No. 4.3e-40; iive 10; Mismatches 15;
                                                                                                                                                                                        Query Match
Best Local Similarity 77.18
Best Local Similarity 77.18
Conservative
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PIR, PH1105, PH1106

PIR, PH1114, PH1116

PIR, PH1119, PH1118

PIR, PH1126, PH1126

PIR, PH125, PH126

PIR, PH1276, PH126

PIR, PH129, PH127

PIR, PH131, PH131

PIR, PH131, PH131

PIR, PH131, PH131

PIR, PH134, PH1134

PIR, PH144, PH142

PIR, PH144, PH142

PIR, PH144, PH144

PIR, PH149, PH1147

PIR, PH149, PH1147

PIR, PH149, PH1147

PIR, PH151, PH1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=CS7BL/6;
                 SEQUENCE FROM N.A.
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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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T "Direct Estimation of Relative Affinity by Flow Cytometry Reveals

T Affinity Maturation of B Call Antigen Receptors in Response to (4-

Hydroxy-3-Witrophenyl)Acetyl (NP).";

EMBL; AB069917; BAB63933.1; -..

R PIR; PH1156; PH1156;

R PH156; PH1156; PH1156.

R InterPro; IPR00710; Ig-like.

R InterPro; IPR00710; Ig-like.

R PF0071TE; PR007596; Ig-v.

R PF0071TE; PR00406; Igv; 1.

R PROSTTE; PS50815; IG-LIKE; 1.
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                                                                                                                                                                                                                      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Best Local Similarity 76.9%; Score 466.5; DB 11; Length 140;
Best Local Similarity 76.9%; Pred. No. 9.5e-41;
Matches 90; Conservative 10; Mismatches 14; Indels 3;
                                                                                            Length 141;
                                                                                                                                                            Indels
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NON TER 140 140
SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;
141 141
141 AA; 15561 MW; DDD80482D66B76A0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                        Query Match 76.1%; Score 467; DB 11; Best Local Similarity 75.3%; Pred. No. 8.5e-41; Matches 88; Conservative 11; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O924R3;
01-DEC-2001 (TrEMBLrel. 19, Created)
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V23-D-J-C MU.
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PF00047; ig; 1.
SM00406; IGv; 1
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                            Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitropheny)] Acetyl (RP) ";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067787; BAB63272.1; -...
                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.9%; Score 466; DB 11; Length 145; 75.8%; Pred. No. 1.1e-40; ive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
15996 MW; 35B1A36E4280BA81 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0924Q7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
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PIR; PH1108; PH1108.

PIR; PH11109; PH1108.

PIR; PH1119; PH1119.

PIR; PH1128; PH1128.

PIR; PH1128; PH1128.

PIR; PH1129; PH1128.

PIR; PH1131; PH1131.

PIR; PH1131; PH1142.

PIR; PH1142; PH1142.

PIR; PH1142; PH1142.

PIR; PH1143; PH1142.

PIR; PH1143; PH1143.

PIR; PH1143; PH1143.

PIR; PH1150; PH1150.

PIR; PH1150; PH1150.

PIR; PH1151; PH1151.

PIR; PH1151; PH1151.

PIR; PH1153; PH1152.

PIR; PH1153; PH1153.

PIR; S26744; S26744.

INTEAPTO; IPRO07110; IG-1:

INTEAPTO; IPRO07110; IG-1.

SMART; SMO0406; IGV; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 75.8
Matches 91; Conservative
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145 AA;
                                                                                          SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=10090;
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1D 09240
AC 09240
DT 01-DE
DT 01-DE
DT VH186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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A Corono Y., Kozono H., Azuma T.;

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Thirtity Maturation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-
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BY EMBL, AB067393; BAB63278.1; -..

BENEL, AB067393; BAB63278.1; -..

BENEL, PH1105; PH1105.

BIR; PH1105; PH1106.

BIR; PH1105; PH1126.

BIR; PH1126; PH1126.

BIR; PH1127; PH1127.

BIR; PH1137; PH1137.

BIR; PH1147; PH1147.

BIR; PH1147; PH1144.

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BIR; PH1150; PH1151.

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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16141 MW; 55A59A7908B2CD6A CRC64;
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PROSITE; PS50835; IG_LIKE; 1.
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89; Conservative
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DR EMBL, AB067789; BAB63274.1; -.

DR PIR, PR3332 F3392.

DR PIR, PH105; PH106.

DR PIR, PH1105; PH1106.

DR PIR, PH1105; PH1106.

DR PIR, PH1129; PH1106.

DR PIR, PH1129; PH1129.

DR PIR, PH1129; PH1129.

DR PIR, PH1129; PH1129.

DR PIR, PH1129; PH1129.

DR PIR, PH1137; PH1131.

DR PIR, PH1137; PH1137.

DR PIR, PH1377; PH1137.

DR PIR, PH1377;
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